

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:55:09 ; Search time 194 Seconds
(without alignments)
625.794 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGGQGPFRQECGEPAIP.....LVVLGVLLGQFVWRPFKS 211

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	1 BAK_HUMAN	Q16611 homo sapien
2	1103	100.0	211	2 CAG33700	Cag33700 homo sapi
3	1075	97.5	211	1 BAK2_HUMAN	Q13014 homo sapien
4	977.5	88.6	190	2 O8NF3	O8NF3 homo sapien
5	845	76.6	209	2 O8C264	O8C264 mus musculus
6	839	76.1	209	2 O9JX59	O9JX59 rattus norv
7	829.5	75.2	208	1 BAK_MOUSE	O08734 mus musculus
8	733	66.5	163	2 O9MZS6	O9MZS6 ovis aries
9	452	41.0	151	2 O91WX5	O91WX5 mus musculus
10	452	41.0	151	2 AAH57589	AAH57589 mus muscu
11	390	35.4	80	2 O77738	O77738 sus scrofa
12	189	17.1	239	1 BCL2_HUMAN	P10415 homo sapien
13	186	16.9	239	1 BCL2_BOVIN	O02718 bos taurus
14	184	16.7	239	1 BCLX_CHICK	Q00709 gallus gall
15	183.5	16.6	233	1 BCLX_CHICK	O9W6F1 gallus gall
16	181	16.4	211	2 O9W6F1	O9W6F1 gallus gall
17	181	16.4	217	2 O99N35	O99N35 mus musculus
18	181	16.4	233	1 BCLX_MOUSE	O64373 mus musculus
19	181	16.4	233	1 BCLX_RAT	P53563 rattus norv
20	181	16.4	233	2 O9MYW4	O9MYW4 oryctolagus
21	180.5	16.4	199	2 O8C5P0	O8C5P0 mus musculus
22	180	16.3	201	2 O6GI15	O6GI15 xenopus tro
23	180	16.3	233	1 BCLX_HUMAN	O07817 homo sapien
24	180	16.3	233	2 O76LT7	O76LT7 canis fami
25	180	16.3	233	2 O9MZS7	O9MZS7 ovis aries
26	180	16.3	233	2 O8SQ42	O8SQ42 felis silve
27	180	16.3	233	2 BAB71819	BAB71819 canis fam
28	180	16.3	233	2 AAP35872	AAP35872 homo sapi
29	180	16.3	239	2 Q75SV7	Q75SV7 canis fami
30	180	16.3	239	2 BAD05044	BAD05044 canis fam
31	179.5	16.3	236	1 BCL2_MOUSE	P10417 mus musculus

ALIGNMENTS

RESULT 1

BAK_HUMAN	178.5	16.2	236	1	BCL2_RAT	P49950 rattus norv
AC Q16611; Q92533;	177.5	16.1	236	2	Q7TSN8	Q7TSN8 rattus norv
DT 01-NOV-1997 (Rel. 35, Created)	177.5	16.1	236	2	Q8BQK4	Q8BQK4 mus musculus
DT 01-NOV-1997 (Rel. 35, Last sequence update)	177.5	16.1	236	2	Q923R6	Q923R6 cricetus
DT 01-OCT-2004 (Rel. 45, Last annotation update)	177.5	16.1	236	2	Q9N1A2	Q9N1A2 sus scrofa
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK) (BCL2-like 7 protein).	176.5	16.0	199	2	O6NTH7	O6NTH7 mus musculus
GN Name=BAK1; Synonyms=BAK, BCL2L7;	176.5	16.0	199	2	AAH68988	AAH68988 mus muscu
OS Homo sapiens (Human)	176.5	16.0	180	2	Q8BDD5	Q8BDD5 bos taurus
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	176	16.0	193	1	BCLW_HUMAN	BCLW_HUMAN homo sapien
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	176	16.0	233	1	BCLX_PIG	O77737 sus scrofa
OX NCBI_TaxID=9606;	175	15.9	235	2	Q81008	Q81008 felis silve
RN [1]	174	15.8	180	2	Q9BDX7	Q9BDX7 bos taurus
RP SEQUENCE FROM N.A.	173.5	15.7	236	2	O6R755	O6R755 canis fami
RC TISSUE=B-cell;	173.5	15.7	236	2	AA92491	AA92491 canis fam
RX MEDLINE=95231652; PubMed=7715729;						
RA Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,						
RA Grinham C.J., Martinou J.C., Brown R.;						
RT "Cloning of a bcl-2 homologue by interaction with adenovirus E1B						
RT 19K.;"						
RL Nature 374:731-733 (1995).						
RN [2]						
RP SEQUENCE FROM N.A.						
RX MEDLINE=95231653; PubMed=7715730;						
RA Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,						
RA Evan G.I., Guild B.C.;						
RT "Induction of apoptosis by the Bcl-2 homologue Bak.;"						
RL Nature 374:733-736 (1995).						
RN [3]						
RP SEQUENCE FROM N.A.						
RX MEDLINE=95231654; PubMed=7715731;						
RA Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,						
RA Tomei L.D., Barr P.J.;						
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue						
RT Bak.;"						
RL Nature 374:736-739 (1995).						
RN [4]						
RP SEQUENCE FROM N.A., AND VARIANTS VAL-28 AND ARG-69.						
RX Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,						
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,						
RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;						
RT "NIHES-SNFs, environmental genome project, NIHES ES15478, Department						
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";						
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.						
RN [5]						
RP SEQUENCE FROM N.A.						
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;						
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,						
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,						
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,						
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,						
RA Babbage A.K., Baggeley C.L., Bailey J., Banerjee R., Barker D.J.,						

RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
 RA Culler K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.O.,
 RA Gibby L.M., Gilson C.J., Githero R.J., Graham D.V., Grant M.,
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hallis K.S.,
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 RA Porter X.M., Ramsey V., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
 RA Schra H.K., Sheridan B., Skuce C.B., Smith S., Smith M., Straggion L.,
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 RA Theaker A.G., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
 RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
 RT "The DNA sequence and analysis of human chromosome 6";
 RL Nature 425:805-811 (2003).
 RN [6]
 RN SEQUENCE FROM N.A.
 RN TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins J.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan M., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schaeetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalish D.E.,
 RA Scherch A.J., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [7]
 RN SEQUENCE OF 96-206 FROM N.A.
 RA Eguchi H., Hayashi S.;
 RT "Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and
 cancer cells.";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RN MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
 RX MEDLINE=96091131; PubMed=8521816;
 RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
 RA Elangovan B., Chinnadurai G., Lutz R.J.;
 RT "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell
 death and protein binding functions.";
 RL EMBO J. 14:5589-5596 (1995).
 RN [9]
 RN STRUCTURE BY NMR OF 72-87.
 RX MEDLINE=97172562; PubMed=9020082;
 RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,

RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
 RA Thompson C.B., Feick S.W.;
 RT "Structure of Bcl-xL-Bak peptide complex: recognition between
 regulators of apoptosis.";
 RL Science 275:983-986 (1997).
 CC -1- FUNCTION: In the presence of an appropriate stimulus, accelerates
 programmed cell death by binding to, and antagonizing the a
 repressor Bcl-2 or its adenovirus homolog E1B 19K protein.
 CC -1- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19K protein, and Bcl-
 X(L).
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with
 highest levels in the heart and skeletal muscle.
 CC -1- DOMAIN: Inactive BH3 domain is required by BIK, BID, BAK, BAD and
 BAX for their pro-apoptotic activity and for their interaction
 with anti-apoptotic members of the Bcl-2 family.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -----
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 CC -----
 DR EMBL; X84213; CAAS8997.1; -;
 DR EMBL; U23765; AAA33066.1; -;
 DR EMBL; U16811; AAA74466.1; -;
 DR EMBL; AY260471; AAC74828.1; -;
 DR EMBL; Z93017; CAB56526.1; -;
 DR EMBL; BC004431; AAH04431.1; -;
 DR EMBL; D83397; BAA13606.1; -;
 DR EMBL; D88396; BAA13606.1; JOINED.
 DR PIR; S58873; S58873.
 DR PDB; 1BXL; NMR; B=72-87.
 DR Genew; HGNC:949; BAK1.
 DR MIM; 600516; -;
 DR GO; GO:0008637; P.apoptotic mitochondrial changes; TAS.
 DR InterPro; IPR00712; BCL2_BH.
 DR Pfam; PF00452; Bcl-2; 1.
 DR PROSITE; PS00662; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR 3D-structure; Apoptosis; Polymorphism; Transmembrane.
 FT DOMAIN 74 88
 FT BH3.
 FT DOMAIN 117 136
 FT BH1.
 FT DOMAIN 169 184
 FT TRANSMEM 188 205
 FT VARIANT 28 28
 FT A -> V.
 FT VARIANT 69 69
 FT /FTID=VAR_018829.
 FT S -> R.
 FT /FTID=VAR_018930.
 FT TURN 74 75
 FT HELIX 76 84
 FT TURN 85 85
 FT TURN 85 85
 SQ SEQUENCE 211 AA; 23409 MW; A2200FE72A46D04E CRC64;
 Query Match 100.0%; Score 1103; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 4.4e-90;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGGQGGPPROECGEPALPSASEEQVAQDTEVFVFRVYHQQEAGVAAAPADPEM 60
 DB 1 MASGGQGGPPROECGEPALPSASEEQVAQDTEVFVFRVYHQQEAGVAAAPADPEM 60
 QY 61 VTLPQPSMTGQVGRQLAIIIGDDINRRYDSFQTMLOHQLQTAENAYEYFKIATSLPE 120

Db 61 VTLPLQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALGFGYRLALHYVYOHGLTGLFGQVTRFVDFMLHHCIAEWIAQRGGWAA 180
Db 121 SGINWGRVVALGFGYRLALHYVYOHGLTGLFGQVTRFVDFMLHHCIAEWIAQRGGWAA 180
QY 181 LNLNGSPILNLVVLGVLLGQFVVRFFKS 211
Db 181 LNLNGSPILNLVVLGVLLGQFVVRFFKS 211

RESULT 2
ID CAG33700 PRELIMINARY; PRT; 211 AA.
AC CAG33700; (Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE BAK1 protein.
GN BAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
vector (pDONR201)";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR457419; CAG33700.1; -.
SQ SEQUENCE 211 AA; 23409 MW; A2200FE72A46D04E CRC64;

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.4e-90;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGGPPRQCGEGEPALPSASEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAADPEM 60
Db 1 MASGGGPPRQCGEGEPALPSASEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAADPEM 60

QY 61 VTLPLQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120
Db 61 VTLPLQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVVALGFGYRLALHYVYOHGLTGLFGQVTRFVDFMLHHCIAEWIAQRGGWAA 180
Db 121 SGINWGRVVALGFGYRLALHYVYOHGLTGLFGQVTRFVDFMLHHCIAEWIAQRGGWAA 180

QY 181 LNLNGSPILNLVVLGVLLGQFVVRFFKS 211
Db 181 LNLNGSPILNLVVLGVLLGQFVVRFFKS 211

RESULT 3
ID BAK2 HUMAN STANDARD; PRT; 211 AA.
AC Q13014;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator
BAK-2).
GN Name=BCL2L7P1; Synonyms=BAK2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95231654; PubMed=7715731;
RA Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA Tomei L.D., Barr P.J.;

RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue
Bak.";
RL Nature 374:736-739(1995).
CC -!- FUNCTION: In the presence of an appropriate stimulus, accelerates
programmed cell death by binding to, and antagonizing the a
repressor Bcl-2 or its adenovirus homolog E1B 19k protein.
CC -!- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19k protein, and Bcl-
X(L).
CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with
highest levels in the heart and skeletal muscle.
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and
BAX for their pro-apoptotic activity and for their interaction
with anti-apoptotic members of the Bcl-2 family. Apoptotic members
of the Bcl-2 family.
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- CAUTION: This is probably the product of a pseudogene.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U16812; AAA74467.1; -.
DR PIR; S58875; S58875.
DR HSSP; Q16611; 1BXL.
DR Genew; HGNC:996; BCL2L7P1.
DR GO; GO:0016020; C:membrane; NAS.
DR GO; GO:0006917; P:induction of apoptosis; NAS.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF0452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
KW Apoptosis; Hypothetical protein; Transmembrane.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 Potential.
SQ SEQUENCE 211 AA; 23411 MW; 703875EC4DCC1D3 CRC64;

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 1.4e-87;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQCGEGEPALPSASEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAADPEM 60
Db 1 MASGGGPPRQCGEGEPALPSASEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAADPEM 60

QY 61 VTLPLQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120
Db 61 VTLPLQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVVALGFGYRLALHYVYOHGLTGLFGQVTRFVDFMLHHCIAEWIAQRGGWAA 180
Db 121 SGINWGRVVALGFGYRLALHYVYOHGLTGLFGQVTRFVDFMLHHCIAEWIAQRGGWAA 180

QY 181 LNLNGSPILNLVVLGVLLGQFVVRFFKS 211
Db 181 LNLNGSPILNLVVLGVLLGQFVVRFFKS 211

RESULT 4
QGNFF3

```

ID Q8NFF3 PRELIMINARY; PRT; 190 AA.
AC Q8NFF3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pro-apoptotic protein BAKN variant.
GN Name=BAK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Ma J.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF520590; AAM74949.1; -.
DR HSP; Q16611; 1BXI.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 190 AA; 21231 MW; A9D4EB8526D0897B CRC64;

Query Match 88.6%; Score 977.5; DB 2; Length 190;
Best Local Similarity 90.0%; Pred. No. 5.9e-79;
Matches 190; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 MASGGGPGPPRQCEGPEPALPSASEQVAQDTSEVRSYVYFHQOEQAEGVAAPADPEM 60
DB 1 MASGGGPGPPRQCEGPEPALPSASEQVAQDTSEVRSYVYFHQO----- 44

QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 45 -----QPSSTMGQVGRQLAIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 99

QY 121 SGINGRVVALLGFGYRLALHYQHLGTLGQVTRFVVDPMHLHICARWIAORGWVAA 180
DB 100 SGINGRVVALLGFGYRLALHYQHLGTLGQVTRFVVDPMHLHICARWIAORGWVAA 159

QY 181 LNLGNPILNLVLGLGVLGLGQVVRFRPKS 211
DB 160 LNLGNPILNLVLGLGVLGLGQVVRFRPKS 190

RESULT 5
Q8C264 PRELIMINARY; PRT; 209 AA.
ID Q8C264;
AC Q8C264;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone:F63004J23 product:BCL2-
DE antagonist/killer 1, full insert sequence.
GN Name=Bak1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Carninci P.;
RL MEDLINE=99279253; PubMed=10349636;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
SEQUENCE FROM N.A.

RC STRAIN=NOD;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K.; Itoh M.; Aizawa K.; Nagaoka S.; Sasaki N.; Carninci P.;
RA Konno H.; Akiyama J.; Nishi K.; Kitsuai T.; Tashiro H.; Itoh M.;
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
RA Fujiwara S.; Inoue K.; Ozawa Y.; Izawa M.; Ohara E.; Watahiki M.;
RA Yoneda Y.; Ishikawa T.; Tanaka T.; Matsuura S.; Kawai J.;
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.;
RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.;
RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hiraoka T.; Hirozane T.;
RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.;
RA Katoh H.; Kawai J.; Kojima Y.; Kondo S.; Konno H.; Kouda M.; Koya S.;
RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.;
RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohsato N.; Okazaki Y.;
RA Saito R.; Saitoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.;
RA Sasaki D.; Shibata K.; Shingawa A.; Shiraki T.; Sugabe Y.; Tagami M.;
RA Tsegawa A.; Takahashi F.; Takaku-Akanha S.; Takeda Y.; Tanaka T.;
RA Tomaru A.; Toya T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089220; BAC40796.1; -.
DR HSP; Q16611; 1BXL.
DR MGD; MGI:1057161; Bak1.
DR GO; GO:0008635; P:caspace activation via cytochrome c; IMP.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 209 AA; 23234 MW; 55E72D29A8AFD18 CRC64;

Query Match 76.6%; Score 845; DB 2; Length 209;
Best Local Similarity 76.8%; Pred. No. 4.3e-67;
Matches 162; Conservative 21; Mismatches 26; Indels 2; Gaps 1;

QY 1 MASGGGPGPPRQCEGPEPALPSASEQVAQDTSEVRSYVYFHQOEQAEGVAAPADPEM 60
DB 1 MASGGGPGPPKVGCDSE--PSSEQVAQDTSEVRSYVYFHQOEQAEGVAAPADPEM 58
QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
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Db 59 DNLFLEPNSILQVGRQALIGDDINRRYDTFQNLLEQLQPTAGNAYELFTKIASLFLK 118
Qy 121 SGINWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 180
Db 119 SGISWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 178
Qy 181 LNLGNGPILNLVVLGVLLGQVFRFFKS 211
Db 179 LNLRRDPILSVVIFGVLLGQVFRFFRS 209

RESULT 6
Q9UK59 PRELIMINARY; PRT; 209 AA.
AC Q9UK59
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation."
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL; AF259504; AAF71760.1; -.
DR HSP; Q16611; IBLX.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR007112; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; UNKNOWN_1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 209 AA; 23153 MW; 2493B814B1972421 CRC64;

Query Match 76.1%; Score 839; DB 2; Length 209;
Best Local Similarity 77.3%; Pred. No. 1.5e-66;
Matches 163; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MASGQGPGRQCEGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPADPEM 60
Db 1 MASGQGPGRQCEGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPANPEM 58
Qy 61 VTLPQSSSTMGQVGRQALIGDDINRRYDSEFTQMLQHLQPTAENAYEFTKIATSLFE 120
Db 59 DNLSLEPNSILQVGRQALIGDDINRRYDSEFTQMLQHLQPTAENAYEFTKIATSLFEK 118
Qy 121 SGINWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 180
Db 119 SGISWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 178
Qy 181 LNLGNGPILNLVVLGVLLGQVFRFFKS 211
Db 179 LNLRRDPILSVVIFGVLLGQVFRFFRS 209

RESULT 7
BAK_MOUSE STANDARD; PRT; 208 AA.
AC Q08734;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation."
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL; AF259504; AAF71760.1; -.
DR HSP; Q16611; IBLX.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR007112; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; UNKNOWN_1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 209 AA; 23153 MW; 2493B814B1972421 CRC64;

Query Match 75.2%; Score 829.5; DB 1; Length 208;
Best Local Similarity 76.3%; Pred. No. 1e-65;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

Qy 1 MASGQGPGRQCEGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPADPEM 60
Db 1 MASGQGPGRQCEGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPANPEM 57
Qy 61 VTLPQSSSTMGQVGRQALIGDDINRRYDSEFTQMLQHLQPTAENAYEFTKIATSLFE 120
Db 59 DNLPLEPNSILQVGRQALIGDDINRRYDSEFTQMLQHLQPTAENAYEFTKIATSLFEK 117
Qy 121 SGINWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 180
Db 118 SGISWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 177
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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN Name=BAK1; Synonyms=Bak;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss; TISSUE=Liver;
RX MEDLINE=97446138; PubMed=9299236;
RA Ulrich E., Kauffmann-Zen A., Hueber A.O., Williamson J.,
RA Chittenden T., Ma A., Evan G.I.;
RT "Gene structure, cDNA sequence, and expression of murine Bak, a
RT proapoptotic Bcl-2 family member."
RL Genomics 44:195-200(1997).
CC -!- FUNCTION: In the presence of an appropriate stimulus, accelerates
CC programmed cell death by binding to, and antagonizing the a
CC repressor Bcl-2 or its adenovirus homolog E1B 19K protein (By
CC similarity).
CC -!- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19K protein, and Bcl-
CC X(L) (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family (By similarity).
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; Y13231; CAA73884.1; -.
DR HSP; Q16611; IBLX.
DR MGD; MGI:1097161; Bak1.
DR GO; GO:0008635; P:caspase activation via cytochrome c; IMP.
DR InterPro; IPR007112; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
KW Apoptosis; Transmembrane.
FT DOMAIN 71 85 BH3.
FT DOMAIN 114 133 BH1.
FT DOMAIN 166 181 BH2.
FT TRANSMEM 185 202 Potential.
SQ SEQUENCE 208 AA; 23300 MW; DAFCl1B160C523C9 CRC64;

Query Match 75.2%; Score 829.5; DB 1; Length 208;
Best Local Similarity 76.3%; Pred. No. 1e-65;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

Qy 1 MASGQGPGRQCEGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPADPEM 60
Db 1 MASGQGPGRQCEGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPANPEM 57
Qy 61 VTLPQSSSTMGQVGRQALIGDDINRRYDSEFTQMLQHLQPTAENAYEFTKIATSLFE 120
Db 59 DNLPLEPNSILQVGRQALIGDDINRRYDSEFTQMLQHLQPTAENAYEFTKIATSLFEK 117
Qy 121 SGINWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 180
Db 118 SGISWGRVALLGFGYRLALHYVQGLTGFGLQVTRFVDFMLHHCIAEWIAQGGWAA 177
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA);
RC STRAIN=CS7BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC057589; AAH57589.1; -. 18C13BPF86E4F33B CRC64;
SQ SEQUENCE 151 AA; 16402 MW; 18C13BPF86E4F33B CRC64;

Query Match
Best Local Similarity 41.0%; Score 452; DB 2; Length 151;
Matches 87; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

QY 1 MASGQGGPPRQCGEPALPSAEEQVAQDTEVFRSYFYRHQCFQAEAGVAAADPDM 60
Db 1 MASGQGGPPKVCDDSS--PSPSEQVAQDTEVFRSYFYRHQCFQAEAGVAAADPDM 58
QY 61 VTLPSPSTMGVQGLALIGDINRRYDSEFTMLQHLQPTAENAYEFTFKIAT 116
Db 59 DNLPLEPNSILGQVQGLALIGDINRRYDTEFTQNLLEQLQPTAGNAYLFTFKIAS 114

RESULT 11
O77738 PRELIMINARY; PRT; 80 AA.
ID O77738
AC O77738
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Bak protein (Fragment).
GN Name=bak;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1];
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ001204; CA04598.1; -.
DR GO: GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro: IPR000712; Bcl2 BH
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS00662; BCL2_FAMILY; 1.
DR PROSITE: PS01259; BH3; 1.
FT NCN TER 1
FT NCN TER 80
SQ SEQUENCE 80 AA; 8818 MW; F01A983B7D59C86 CRC64;

Query Match
Best Local Similarity 35.4%; Score 390; DB 2; Length 80;
Matches 74; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 50 EGVAAPADPEMVTLPQPSSTMGVQGLALIGDINRRYDSEFTMLQHLQPTAENAYE 109
Db 1 DGAAPADPEMVTLPQPSSTMGVQGLALIGDINRRYDSEFTMLQHLQPTAENAYE 60

QY 110 YFTKIATSLFESGINWGRV 129
Db 61 YFTKIATSLFESGINWGRV 80

RESULT 12
BCL2_HUMAN
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q13842; Q16197;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN Name=BCL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of bcl-
RT 2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2];
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT 2/immunoglobulin transcript resulting from the t(14;18)
RT translocation.";
RL Cell 47:19-28(1986).
RN [4];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation of
RT the Bcl-2-Ig fusion gene in lymphoma.";
RL EMBO J. 7:1123-131(1988).
RN [5];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witral L.A., Nickerson D.A.;
RT "NIHNS-SNPs, environmental genome project, NIHNS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [6];
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramo R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield J.S.N., Krzyzinski M.L., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [7]

RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS

RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILS-93.

RA MEDLINE=92096610; PubMed=1339299;

RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;

RT "Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-Hodgkin's lymphomas.";

RL Blood 79:229-237(1992).

RN [8]

RP SUBCELLULAR LOCATION.

RP MEDLINE=91066924; PubMed=2250705;

RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;

RT "Bcl-2 is an inner mitochondrial membrane protein that blocks programmed cell death.";

RL Nature 348:334-336(1990).

RN [9]

RP MUTAGENESIS.

RP MEDLINE=94239528; PubMed=8183370;

RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;

RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of apoptosis and heterodimerization with Bax.";

RL Nature 369:321-323(1994).

RN [10]

RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.

RP MEDLINE=98057466; PubMed=9395403;

RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A., Ueno K., Hardwick J.M.;

RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";

RL Science 278:1966-1988(1997).

RN [11]

RP INTERACTION WITH TP53BP2.

RP MEDLINE=96251339; PubMed=8668206;

RA Naumovski L., Cleary M.L.;

RT "The p53-binding protein 53BP2 also interacts with Bcl2 and impedes cell cycle progression at G2/M.";

RL Mol. Cell. Biol. 16:3884-3892(1996).

RN [12]

RP REVIEW ON PHOSPHORYLATION.

RP MEDLINE=21260650; PubMed=11368354;

RA Ruvoilo P.P., Deng X., May W.S.;

RT "Phosphorylation of Bcl2 and regulation of apoptosis.";

RL Leukemia 15:515-522(2001).

RN [13]

RP PHOSPHORYLATION BY ASK1/JNK1.

RP MEDLINE=20036804; PubMed=10567572;

RA Yamamoto K., Ichijo H., Korsmeyer S.J.;

RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal protein kinase pathway normally activated at G2/M.";

RL Mol. Cell. Biol. 19:8469-8478(1999).

CC -I- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).

CC -I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1, RAP-1 and TP53BP2.

CC -I- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

CC -I- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Alpha;

CC IsoId=PI0415-1; Sequence=Displayed;

CC Name=Beta;

CC IsoId=PI0415-2; Sequence=VSP_000512;

CC TISSUE SPECIFICITY: Expressed in a variety of tissues.

CC -I- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAP-1.

CC -I- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).

CC -I- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

CC -I- DISEASE: Involved in follicular lymphoma (FL) (also known as type II chronic lymphatic leukemia) by a chromosomal translocation t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying the chromosomal translocation could be attributed to the Ig somatic hypermutation mechanism resulting in nucleotide transitions.

CC -I- SIMILARITY: Belongs to the Bcl-2 family.

CC -I- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

CC -I- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

CC -I- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

CC -I- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

CC -I- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;/BCL2ID49.html". WWW="http://www.infobiogen.fr/services/chromancer/Genes/BCL2ID49.html".

CC -----

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CC -----

CC EMBL; M13994; AA51813.1; ALT_SEQ.

CC EMBL; M13995; AA51814.1; ALT_SEQ.

CC EMBL; M14745; AA35591.1; -.

CC EMBL; X06487; CAA29778.1; -.

CC EMBL; AY220759; AAC26045.1; -.

CC EMBL; BC027258; AA27258.1; -.

CC EMBL; S72602; AAD14111.1; ALT_SEQ.

CC PIR; B29409; TVHUB1.

CC PIR; C37332; TVHUA1.

CC PDB; 1G5W; NMR; A=3-48.

CC PDB; 1GJH; NMR; A=3-48.

CC IntAct; F10415; -.

CC Genew; HGNC:990; BCL2.

CC MIM; 151430; -.

CC GO; GO:0005741; C:mitochondrial outer membrane; NAS.

CC GO; GO:0005515; F:protein binding; TAS.

CC GO; GO:0006916; P:anti-apoptosis; TAS.

CC GO; GO:0006959; P:humoral immune response; TAS.

CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.

CC GO; GO:0000074; P:regulation of cell cycle; TAS.

CC InterPro; IPR000712; Bcl2_BH.

Query March 17.18; Score 189; DB 1; Length 239;

Best Local Similarity 26.4%; Pred.No. 1.5e-08;

Matches 58; Conservative 81; Indels 50; Gaps 8;

30 DTEVFVRSYVYFRHQQ---EQAEGV-----AAPA-----DPMVT 62

|||

Db 10 DNREIVMKYHYKLSQRYEWADGVGAAPGAPAFISQFQHTPHPAASRDPVART 69
 Qy 63 LPLO-PSSTMGQVGRQIAI-----GDDINERYDSBFTMLQHLQPTAENAYEY 110
 Db 70 SPLQTPAAGAAAGPALSPPVPHVLTIRQAGDDFSRRYRDFAEMSSQLHLTPFTARGR 129
 Qy 111 FTKIATSLFSGINWGRVALLGFGYRLALHVQHGLTGFLGQVTRFVDFMLHHCIAWR 170
 Db 130 FATVEELFDGVMNGRIVAFEFEGGVMCVSNREMSPLVDNIALMWTLYLNRH-LHTW 188
 Qy 171 IAQRGGWVAALNNGNPI-----LNVLVGLGVVLLG 201
 Db 189 IQDNGGWDFAVEL-YGFSMRPLDFSWLSKLLSLALVG 227

RESULT 13

BCL2_BOVIN
 ID_BCL2_BOVIN STANDARD; PRT; 229 AA.
 AC O02718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 03-JUL-2004 (Rel. 44, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN Name=BCL2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein; TISSUE=Thymus;
 RX MEDLINE=98162580; PubMed=9501056;
 RA Reyes R.A., Cockerell G.L.;
 RT "Increased ratio of bcl-2/bax expression is associated with bovine
 leukemia virus-induced leukemogenesis in cattle.";
 RL Virology 242:184-192(1998).
 CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 permeability. Appears to function in a feedback loop system with
 caspases. Inhibits caspase activity either by preventing the
 release of cytochrome c from the mitochondria and/or by binding to
 the apoptosis-activating factor (APAF-1) (By similarity).
 CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
 domains, and is necessary for anti-apoptotic activity. Also
 interacts with APAF-1, RA1 and IFSBP2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 membrane of the nuclear envelope and the endoplasmic reticulum (By
 similarity).
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 for interaction with RA1-1 (By similarity).
 CC -!- PTM: Phosphorylation/dephosphorylation on Ser-63 regulates Bcl2
 anti-apoptotic activity. Growth factor-stimulated phosphorylation
 on Ser-63 by PKC is required for the anti-apoptosis activity and
 occurs during the G2/M phase of the cell cycle (By similarity). In
 the absence of growth factors, Bcl2 appears to be phosphorylated
 by other protein kinases such as ERKs and stress-activated
 kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
 similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 cleaved protein, lacking the BH4 domain, has pro-apoptotic
 activity, causes the release of cytochrome c into the cytosol
 promoting further caspase activity (By similarity).
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

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CC EMBL; U92434; AAB53319.1; .
 DR HSP; P10415; 1GJH.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_Family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS00062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS00063; BH4_2; 1.
 KW Apoptosis; Mitochondrion; Phosphorylation; Transmembrane.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 64 68 Poly-Pro.
 FT DOMAIN 69 72 Poly-Ala.
 FT DOMAIN 83 97 BH3.
 FT DOMAIN 126 145 BH1.
 FT DOMAIN 177 192 BH2.
 FT TRANSMEM 202 223 Potential.
 FT SITE 34 35 Cleavage (by caspases) (By similarity).
 FT MOD_RES 53 63 Phosphoserine (by PKC) (By similarity).
 SQ SEQUENCE 229 AA; 25099 MW; AD1DD0AF98FF11D CRC64;

Query Match 16.9%; Score 186; DB 1; Length 229;
 Best Local Similarity 26.2%; Pred. No. 2.6e-08;
 Matches 55; Conservative 30; Mismatches 85; Indels 40; Gaps 7;

Qy 30 DTEVFVSRYFYRHQ---PQAEGV-----AAPAD-----PEMVTLPQPS 68
 Db 10 DNREIVMKYHYKLSQRYEWADGVGAAPGAPAFISQFQHTPHPAASRDPVART 69
 Qy 69 STMQ-----YGRQLAIGDDINRYDSEFQTLQHLQPTAENAYEYFTKIATSLPE 120
 Db 70 AAQAPSPVPPVPHVLTIRQAGDDFSRRYRDFAEMSSQLHLTPFTARGRFAIVVEELFR 129
 Qy 121 SGINWGRVALLGFGYRLALHVQHGLTGFLGQVTRFVDFMLHHCIAWRVIAQRGGWVA 180
 Db 130 DGVNMGRIVAFEFEGGVMCVSNREMSPLVDNIALMWTLYLNRH-LHTWIDQNGGWDFA 188
 Qy 181 LNLGNGPI-----LNVLVGLGVVLLG 201
 Db 189 VEL-YGFSMRPLDFSWLSKLLSLALVG 217

RESULT 14

BCLX_CHICK
 ID_BCLX_CHICK STANDARD; PRT; 229 AA.
 AC O07816; Q98908;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN Name=BCL2l1; Synonym=BCLX, BCL-X;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=93364977; PubMed=8358789;
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.;

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CC or send an email to license@isb-sib.ch).
CC -----

CC EMBL; D11382; BAA01978.1; --
DR EMBL; D11381; BAA01978.1; JOINED.
DR EMBL; Z11961; CAA78018.1; --
DR PIR; A37332; A37332.
DR PIR; S24390; S24390.
DR HSP; P10415; IGSM.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Transmembrane.
FT DOMAIN 10 30 BH4.
FT DOMAIN 87 101 BH3.
FT DOMAIN 130 149 BH1.
FT DOMAIN 181 196 BH2.
FT TRANSMEM 208 228 Potential.
FT CONFLICT 64 64 E -> S (in Ref. 2).
FT CONFLICT 67 82 GSAASEVPPAELRP -> ARLLVRCPLRGCA (in
FT Ref. 2).
FT CONFLICT 121 121 H -> T (in Ref. 2).
FT CONFLICT 139 139 G -> V (in Ref. 2).
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6E4C3D CRC64;

Query Match 16.6%; Score 183.5; DB 1; Length 233;
Best Local Similarity 26.9%; Pred. No. 4.4e-08;
Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

QY 2 ASSGG-PGPRCEGCEPALPSASEEQVAQDTEEVRSYVFYRHQQEQEAGVAAAPADPE 59
Db 31 AGEDRPVPFP-----APA-PAAPAAVA-----AAGASSHRRPEPPGSAASEVPPA 77
QY 60 MVTLPQPSSTMGQGRQLAI--IGDDINRRYDSEFQTMLOHQPATAENAYEFTKIATS 117
Db 78 EGLRPAPP-----GVHLALRQAGDEFSRRYQDFQMSGQLHLPFTAHGFRVAVVEE 130
QY 118 LFESGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGW 177
Db 131 LFRDGVNWRGRIVAFFEFGGVMCVESYNREMSPLVDNIATMTTEYLNRH-LHNWIQDNGW 189
QY 178 VAALNL-GNG--PI-----INVLVLGVLIG 201
Db 190 DAFVELYGNRMRLPFDFFSWLSKLTLSLVIG 221

Search completed: December 6, 2004, 16:11:48
Job time : 196 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 16:03:06 ; Search time 38 Seconds
(without alignments)
534.256 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASQGGFPPRQCEGPALP.....LVVLGVLLGQFVRRFKS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	2	Bak protein - huma
2	1075	97.5	211	2	cdn-2 protein - hu
3	189.5	17.2	205	1	transforming prote
4	189	17.1	239	1	transforming prote
5	183.5	16.6	233	2	transforming prote
6	181	16.4	233	2	bcl-x long - mouse
7	181	16.4	233	2	BCL-X long - rat
8	180	16.3	233	2	apoptosis regulato
9	178.5	16.2	199	1	transforming prote
10	177	16.0	236	1	transforming prote
11	176.5	16.0	236	1	gene bcl-2 protein
12	174.5	15.8	216	2	transforming prote
13	173.5	15.7	233	2	transforming prote
14	172.5	15.6	236	2	BCL-X long - rat
15	170.5	15.5	236	2	BCL-2 - rat (fragm
16	167.5	15.2	190	2	apoptosis regulato
17	164	14.9	237	2	apoptosis regulato
18	160.5	14.6	232	2	transforming prote
19	158.5	14.4	214	2	bcl-x transmembran
20	148	13.2	218	2	bcl-2-associated p
21	143.5	13.0	350	2	BCL2 homolog Mcl1
22	143	13.0	192	2	bcl-2-associated p
23	143	13.0	192	2	bcl-2-associated p
24	142	12.9	179	2	Bax-delta protein
25	126	11.4	133	2	bcl-2-associated p
26	122	11.1	154	2	gene bcl-2 protein
27	116	10.5	172	2	hemopoietic-specif
28	112	10.2	175	2	Bcl-2 related - hu
29	109	9.9	143	2	bcl-2-associated p

NR-13 protein - qu
conserved hypothet
Mcl-1a protein - z
cation transportin
cation transportin
dnaj-related prote
band 3-related pro
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypothet
hypothetical prote
odx protein - frui
tenascin-like prot
gop protein - sac
band 3 protein, no

ALIGNMENTS

RESULT 1
S58873
Bak protein - human
N/A:Kernate names: bcl-2 homolog; cdn-1 protein
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S58873; S58872; S58874
R:Chittenden, I.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I.
Nature 374, 733-736, 1995
A>Title: Induction of apoptosis by the Bcl-2 homologue Bak.
A:Reference number: S58873; MUID:95231653; PMID:7715730
A:Accession: S58873
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-211 <CHI>
A:Cross-references: UNIPROT:Q16611; EMBL:X84213; NID:958797; PIDN:AAA93066.1; PID:9758758
R:Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martini
Nature 374, 731-733, 1995
A>Title: Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K.
A:Reference number: S58872; MUID:95231652; PMID:7715729
A:Accession: S58872
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <FAR>
A:Cross-references: EMBL:X84213; NID:9804984; PIDN:CAA58997.1; PID:g804985
R:Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr,
Nature 374, 736-739, 1995
A>Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A:Reference number: S58874; MUID:95231654; PMID:7715731
A:Accession: S58874
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <KIE>
A:Cross-references: EMBL:U16811; NID:g9595923; PIDN:AAA74466.1; PID:g9595924
C:Genetics;
A:Gene: GDB:BAK
A:Cross-references: GDB:635887

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.3e-93;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASQGGFPPRQCEGPALPSAEEQVADTEEVFRSYVFRHQEQEAEQVAAADPEM 60
DB 1 MASQGGFPPRQCEGPALPSAEEQVADTEEVFRSYVFRHQEQEAEQVAAADPEM 60
QY 61 VTLPQSSSTMGVGRQLAIIGDDINRRYDSEFOTMLOHLPQTAENAYEFTKIATSLPE 120
DB 61 VTLPQSSSTMGVGRQLAIIGDDINRRYDSEFOTMLOHLPQTAENAYEFTKIATSLPE 120
QY 121 SGINWRVALLGFGYRLALHYVHGLTGFLGVQVTRFVDFMLHCHICARVIAORGWAA 180

Db 121 SGINGRVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIARWIAQRGGWVAA 180
QY 181 LNLGNGPILNLVLGVLGQVVRFFPKS 211
Db 181 LNLGNGPILNLVLGVLGQVVRFFPKS 211

RESULT 2
S58875
cdn-2 protein - human
C/Species: Homo sapiens (man)
C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S58875
R/Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, Nature 374, 736-739, 1995
A/Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A/Reference number: S58874; MUID:95231654; PMID:7715731
A/Accession: S58875
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-211 <KIE>
A/Cross-references: UNIPROT:Q13014; EMBL:U16812; NID:G595925; PIDN:AAA74467.1; PID:G5959
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match 97.5%; Score 1075; DB 2; Length 211;
Best Local Similarity 97.2%; Pred. No. 2.9e-90;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRCEGPPALPSASEQVADTEEVFRSYVYRHQOEQAEGVAPADPEM 60
Db 1 MASGGGPPRCEGPPALPSASEQVADTEEVFRSYVYRHQOEQAEGVAPADPEM 60

QY 61 VTLPQPSSTMQGVGQQLAIGDDINRRYDSFQTMQLQHTAENAYEYFTKIATSLFE 120
Db 61 VTLPQPSSTMQGVGQQLAIGDDINRRYDSFQTMQLQHTAENAYEYFTKIATSLFE 120

QY 121 SGINGRVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIARWIAQRGGWVAA 180
Db 121 SGINGRVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIARWIAQRGGWVAA 180

QY 181 LNLGNGPILNLVLGVLGQVVRFFPKS 211
Db 181 LNLGNGPILNLVLGVLGQVVRFFPKS 211

RESULT 3
TVHUB1
transforming protein bcl-2, splice form beta - human
N/Alternate names: apoptosis regulator bcl-2
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: B29409; I52566; D37332
R/Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A/Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A/Reference number: A29409; MUID:86259760; PMID:3523487
A/Accession: B29409
A/Molecule type: mRNA
A/Residues: 1-205 <TSU>
A/Cross-references: UNIPROT:P10415; GB:M13995; NID:G179368; PIDN:AAA51814.1; PID:G179369
R/Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.
Blood 79, 229-237, 1992
A/Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-H
A/Reference number: I52566; MUID:92096610; PMID:1339299
A/Accession: I52566
A/Status: translated
A/Molecule type: DNA
A/Residues: 1-131 <TAN>
A/Cross-references: GB:S72602; NID:G241046; PIDN:AADI4111.1; PID:G4261811
R/Tsujimoto, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A/Reference number: A37332; MUID:92375724; PMID:1508712

A/Accession: D37332
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Molecule type: DNA
A/Residues: 1-33, 'E', 34-95, 'T', 97-109, 'R', 111-205 <EGU>
C/Genetics:
A/Gene: GDB:BCL2
A/Cross-references: GDB:119031; OMIM:151430
A/Map position: 18q21.3-18q21.3
C/Function:
A/Description: blocks apoptosis in hematopoietic cells
C/Superfamily: bcl apoptosis regulator, inhibitory type
C/Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 17.2%; Score 189.5; DB 1; Length 205;
Best Local Similarity 27.4%; Pred. No. 8.1e-10;
Matches 54; Conservative 27; Mismatches 73; Indels 43; Gaps 7;

QY 30 DTEEVFRSYVYRHQO---EQEAEGV-----AAPA-----DPEWVT 62
Db 10 DNEIYVKYIHYKLSQRYEWDAGDVGAAPGAPGIFSSQPGHTPHPAASRDVPART 69

QY 63 LPLO-PSSTMQGVGQQLAII-----GDDINRRYDSFQTMQLQHTAENAYEY 110
Db 70 SPLQTPAAPGAAGPALSPVPVHVHALRQAGDFFRRYRGDFAEISSQLHPTPTARGR 129

QY 111 FTKIATSLFESGINGRVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIARW 170
Db 130 FATVVEELFRDGVNMGIVAFEFEGVCMCVSVNREMSPLVDNIALMTEYLNRH-LHTW 188

QY 171 IAORGWVAA---LNLG 184
Db 189 IQDNGGWGASGDVSLG 205

RESULT 4
TVHUB1
transforming protein bcl-2, splice form alpha - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C/Accession: C37332; A29409; S02452; A24428; A27622; B27622
R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A/Reference number: A37332; MUID:92375724; PMID:1508712
A/Accession: C37332
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-239 <EGU>
A/Cross-references: UNIPROT:P10415
A/Note: this report is a correction
R/Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A/Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A/Reference number: A29409; MUID:86259760; PMID:3523487
A/Accession: A29409
A/Molecule type: mRNA
A/Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>
A/Cross-references: GB:M13994; NID:G179366; PIDN:AAA51813.1; PID:G179367
A/Note: this sequence has been corrected in reference A37332
R/Sto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer
EMBO J. 7, 123-131, 1988
A/Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2
A/Reference number: S02452; MUID:88196071; PMID:2834197
A/Accession: S02452
A/Molecule type: mRNA
A/Residues: 1-239 <SET>
R/Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A/Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglob
A/Reference number: A24428; MUID:87002488; PMID:2875799
A/Accession: A24428
A/Molecule type: mRNA
A/Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>

A;C;Cross-references: GB:M14745; NID:q179370; PIDN:AAA35591.1; PID:q179371
A;R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.
OncoGene Res. 2, 263-275, 1998
A;I;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
A;I;Reference number: A27622; MUID:88217344; PMID:3285301
A;Accession: A27622
A;Molecule type: mRNA
A;Residues: 1-58, 'T', 60-239 <HUA>
A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
C;Genetics:
A;Gene: GDB:BCL2
A;Cross-references: GDB:119031; OMIM:151430
A;Map position: 18q21.3-18q21.3
C;Function:
A;Description: blocks apoptosis in hematopoietic cells
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto-

[illegible]

RESULT 5
A33732
transforming protein (bcl-2-alpha) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_number 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A37332; S35453
C:Author: Y.; Ewert, D.L.; Tsujimoto, Y.
C:Nucleic Acids Res. 20, 4187-4192, 1992
C:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
C:Reference number: A37332; MUID:92375724; PMID:1508712
C:Accession: A37332
C:Status: nucleic acid sequence not shown
C:Molecule type: DNA
C:Residues: 1-233 <EGU>
C:Cross-references: UNIPROT:Q00709; EMBL:D11381
C:Genetics:
C:Introns: 189/3
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: Mitochondrion; transforming protein; transmembrane protein

Query Match		16.6%	Score 183.5;	DB 2;	Length 233;	
Best Local Similarity		26.9%;	Pred. No. 3.4e-09;			
Matches	57;	Conservative 35;	Mismatches 87;	Indels 33;	Gaps 10;	
2 ASGGQ--PGP	RQCEGEPALPSAS	EQAQTETEEVFR	VYVYRHOQEQAEGVAAPADPE	59		
:	:	:	:	:	:	
31 AAGEDRPVP-	---APA-PAAAPAAVA---	-----AAGASHHRRPEPPGSAASEVEPPA	77			
:	:	:	:	:	:	
60 MVTLPSPSMTGWGVGR	LAI--IGDDINRRYSDFQTM	LHQPTAEANAYEFTFKIATS	117			
:	:	:	:	:	:	

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78  ECLRPAPP-----GVHLALRQAGDEFRRYQRDFAQMSGQLHLTPTTAHGRFVAVBE 130
QY      118  LPESGINMGVRVALLGFGVRLALHYVHGCLTGFGQVTRFVVDVDFMLHHCIARWIAQRGGW 177
Db      131  LFRDGVNMGRIIVAFPEFGVGWCVESVNREMSPLVDNIATWMTLEYLNRH-LHNWIQDNGW 189
QY      178  VAAALNL-GNG--PI-----LNVLVVLGVVLG 201
Db      190  DAFVELYGNMRLPFDFFSWISLTKILSLVLVG 221

RESULT 6
I49056
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49056; S52866
Ri:fang, W.; Rivard, J.-J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49055; MUID: 95052604; PMID: 7963517

```

A|Accession: I49056
 A|Status: preliminary; translated from GB/EMBL/DBJ
 A|Molecule type: mRNA
 A|Residues: 1-233 <RES>
 A|Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:G506647; PIDN:AAA82173.1; PID:G505
 R|Kanesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
 submitted to the EMBL Data Library, November 1994
 A|Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line thro
 A|Reference number: S52866
 A|Accession: S52866
 A|Status: preliminary
 A|Molecule type: mRNA
 A|Residues: 1-233 <KAM>
 A|Cross-references: EMBL:X83574; NID:G595622; PIDN:CAA58557.1; PID:G595623
 C|Superfamily: bcl apoptosis regulator, inhibitory type

 Query Match 16.4%; Score 181; DB 2; Length 233;
 Best Local Similarity 28.3%; Pred. NO. 5.7e-09;
 Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

```

83  MAAVQALREAGDEPELRYRAFSDLTSQLHITPGTAYQSFQVYNELFRDGVNMGRIVA 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131  LLGFCYRLALHVYQHGLTGFGTQVTRFVVDFMLHHCIARWIAQRCGWAAALNL-GNGP-- 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
143  FFSFGGALCVESVDEKEMQVLVSRTASWMTATYLNDSH-LEPWIQENGGWDTFVDLYGNAAA 201
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
188  -----LNVLVLVGLGVLLGQFVRR 207
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
202  ESRKQGERFNRWFLTGMTVAGVLLGSLFSRK 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
S51761
BCI-X protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51761; S51762
R:Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994

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A:Reference number: S51761
A:Accession: S51761
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MIC>
A:Cross-references: UNIPROT:P53563; EMBL:X82537; NID:G607176; PID:CAA57886.1; PID:G607:
A:Experimental source: embryonic; brain
A:Accession: S51762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255-189-233 <WT>

A:Cross-references: EMBL:X82537; NID:G607176; PIDN:CAA57887.1; PID:G607178
A:Experimental source: embryonic; brain
A:Note: smaller form due to splicing
C:Genetics:
A:Introns: 125/3
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 16.4%; Score 181; DB 2; Length 233;
Best Local Similarity 28.3%; Pred. No. 5.7e-09;
Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

QY 71 MGQVGRQLAIGDINRRYDSFQMLQLOPTANAYEYFKIATSLFESGINRGVVA 130
DB 83 MAAVKQALREAGDEFELRYRAFSDLTSLQHTPTAYQSFQVNVNELFRDGVNNGRIVA 142
QY 131 LLGFGYRLALHYVQHGLTGFLGQVTRFFVVDVFLHHCIARWIAQRCGWVAALNL-GNGP-- 187
DB 143 FFSFGGALCVESVDKEMQVLVSRIASWMTYLNDR-LKPWQENGWDTFVDLYGNNA 201
QY 188 -----ILNVLVVLGVLLGQFVVR 207
DB 202 ESRKQGERFNRWFLTGMTVAGVLLGLSLFSRK 233

RESULT 8

B47537
apoptosis regulator bcl-xL - human
N:Alternate names: bcl-2-related protein
N:Contains: apoptosis regulator bcl-xS
C:Species: Homo sapiens (man)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: B47537; C47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: B47537; MUID:93364977; PMID:8358789
A:Accession: B47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-233 <BO1>
A:Cross-references: UNIPROT:Q07817; GB:L20121; NID:G510900; PIDN:CAA80661.1; PID:G510901
A:Accession: B47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-69, 'G', 71-125, 189-233 <BO2>
A:Cross-references: GB:L20122; NID:G623236; PIDN:CAA80662.1; PID:G623237
C:Genetics:
A:Gene: GDB:BCL2L
A:Cross-references: GDB:228079
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; apoptosis
F:1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F:1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <A2>

Query Match 16.3%; Score 180; DB 2; Length 233;
Best Local Similarity 28.3%; Pred. No. 7e-09;
Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;

QY 71 MGQVGRQLAIGDINRRYDSFQMLQLOPTANAYEYFKIATSLFESGINRGVVA 130
DB 83 MAAVKQALREAGDEFELRYRAFSDLTSLQHTPTAYQSFQVNVNELFRDGVNNGRIVA 142
QY 131 LLGFGYRLALHYVQHGLTGFLGQVTRFFVVDVFLHHCIARWIAQRCGWVAALNL-GNGP-- 187
DB 143 FFSFGGALCVESVDKEMQVLVSRIASWMTYLNDR-LKPWQENGWDTFVDLYGNNA 201

QY 188 -----ILNVLVVLGVLLGQFVVR 207
DB 202 ESRKQGERFNRWFLTGMTVAGVLLGLSLFSRK 233

RESULT 9

TVMSB1

transforming protein bcl-2-beta - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: B25960
R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
A:Reference number: A90893; MUID:87187643; PMID:3032455
A:Accession: B25960
A:Molecule type: DNA
A:Residues: 1-199 <NEG>
A:Cross-references: UNIPROT:P10417; GB:M16506; NID:G468335; PIDN:AAA37281.1; PID:G387110
C:Genetics:
A:Gene: BCL2
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; transforming protein

Query Match 16.2%; Score 178.5; DB 1; Length 199;
Best Local Similarity 25.1%; Pred. No. 7.8e-09;
Matches 49; Conservative 25; Mismatches 84; Indels 37; Gaps 5;

QY 22 ASBEQVAQDTEEVFRSYVFRHQE-----QEAEGVAAP--ADPEWTLPLQP-SSTMGOV 74
DB 2 AQAGRTGYDNRREIVMKYIHYKLSQRYEWDAAGDADAAPLGAAPTGGIFSFQPSNPMPAV 61
QY 75 GRQLAI-----IGDINRRYDSEFQTMQLQHPQTA 105
DB 62 HREMAARTSLPLVATAGPALSVPVPCVHLTRRAGDFFSRYYRDRDPAEMSSQLHLTF 121
QY 106 NAYEYFKIATSLFESGINRGVVALGFGYRLALHYVQHGLTGFLGQVTRFFVVDVFLH 165
DB 122 TARGPATVVEELFRDGVNNGRIVAFEFGGVCMVESVNRMSPLVDNIALMWTYINRH 181
QY 166 CIAEWTAQRCGWAA 180
DB 182 -LHTWIDQNGWVGA 195

RESULT 10

TVMSB1
transforming protein bcl-2-alpha - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
C:Accession: A25960; E37332
R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
A:Reference number: A90893; MUID:87187643; PMID:3032455
A:Accession: A25960
A:Molecule type: DNA
A:Residues: 1-236 <NEG>
A:Cross-references: GB:L31532; GB:M16506; NID:G468336; PIDN:AAA37282.1; PID:G387109
R:Equchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: E37332
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-33, 'E', 34-220, 'AL', 223-236 <EGU>
C:Genetics:
A:Gene: BCL2

A:Introns: 192/3
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 16.0%; Score 177; DB 1; Length 236;
Best Local Similarity 25.1%; Pred. No. 1.3e-08;
Matches 52; Conservative 27; Mismatches 90; Indels 38; Gaps 6;

QY 22 ASBEQVAQDTEEVFRSYVFRHQE-----QEAEGVAAP--ADPEWTLPLQP-SSTMGOV 74
DB 2 AQAGRTGYDNRREIVMKYIHYKLSQRYEWDAAGDADAAPLGAAPTGGIFSFQPSNPMPAV 61

QY 75 GRQLAI-----IGDDINRRYDSEFQTMQLHQPTAE 105
Db 62 HREMAARTSPRLPLVATAGPALSPVPVPCVHLTLRAGDGFSSRRYRRDRFAEMSSQLHLTPF 121
QY 106 NAYEYFTKIATSLFESGINRWGVALLGFGVRLALHVVYQHGLTGLFQGVTRFVVDFMLHH 165
Db 122 TARGRFATVVEELFRDGVNMGRIYVAFPEFGVCMCVSNREMSPLVDNIALMWMTEYLNHR 181
QY 166 CIARWIAQRGGWVAALNLGNPILNVL 192
Db 182 -LHTWIODNGGDFAVEL-YGPSMRPL 206

RESULT 11
153744
Gene bcl-2 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: 153744
R/Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A/Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A/Reference number: 153744; MUID:94193015; PMID:8144041
A/Accession: 153744
A/Molecule type: mRNA
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-236 <RES>
A/Cross-references: UNIPROT:P49950; GB:L14680; NID:G408946; PIDN:AAAS3662.1; PID:G408947
C/Genetics:
A/Gene: bcl-2
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 16.0%; Score 176.5; DB 2; Length 236;
Best Local Similarity 24.2%; Pred. No. 1.5e-08;
Matches 55; Conservative 31; Mismatches 90; Indels 51; Gaps 7;

QY 22 ASEQVAQDTEVFRSVYFRHQ-----EQEAGVAAPA----- 56
Db 2 AQAGRTGYDNKEIWMKYIHKLSQGVYEWDTGDSAPLRAAFTPGIFSQPSNETPAV 61

QY 57 --DPENVTLPLQSSSTMVQVGRQLAI-----GDDINRRYDSEFQTMQLHQPT 103
Db 62 HRDTAARTSPRLP--LVANAGPALSPVPVHVHLTLRAGDGFSSRRYRRDRFAEMSSQLHLT 119

QY 104 AENAYEFTKIATSLFESGINRWGVALLGFGVRLALHVVYQHGLTGLFQGVTRFVVDFML 163
Db 120 PFTARGRFATVVEELFRDGVNMGRIYVAFPEFGVCMCVSNREMSPLVDNIALMWMTEYLN 179

QY 164 HHCIAWIAQRGGWVAALNLGNP-----LNVLVVLGVVLG 201
Db 180 RH-LHTWIODNGGDFAVEL-YGPSMRPLDFSWLSLKTLLSLALVG 224

RESULT 12
B37332
Transforming protein (bcl-2-beta) - chicken
C/Species: Gallus gallus (chicken)
C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C/Accession: B37332; S35452
R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues.
A/Reference number: A37332; MUID:92375724; PMID:1508712
A/Accession: B37332
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-216 <EGU>
A/Cross-references: EMBL:D11381; EMBL:D11382
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 15.8%; Score 174.5; DB 2; Length 216;
Best Local Similarity 27.3%; Pred. No. 2e-08;

Matches 50; Conservative 27; Mismatches 81; Indels 25; Gaps 7;
QY 2 ASQGG--PGPPRQCEGEPALPSASEEQVAQDTEEVFRSVYFRHQEQEAEAGVAAPADPE 59
Db 31 AAGERPPVPP-----APA-PAAPAAVA-----AAGASHHRRPEPPGSAASEVPPA 77
QY 60 MVTLPQSSSTMVQVGRQLAI--IGDDINRRYDSEFQTMQLHQPTAENAYEFTKIATS 117
Db 78 EGLRPAPP-----GVHLAFQAGDEFSRRYQRDFAQMSGQLHLTPPTAHGRFVAVVEE 130
QY 118 LFESGINRWGVALLGFGVRLALHVVYQHGLTGLFQGVTRFVVDFMLHHCIAEWIAQRGGW 177
Db 131 LFRDGVNMGRIYVAFPEFGVCMCVSNREMSPLVDNIALMWMTEYLNHR-LHNWIODNGGW 189
QY 178 VAA 180
Db 190 VEA 192

RESULT 13
167431
BCL-X-Long - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 167431
R/Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A/Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi-constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A/Reference number: 153295; MUID:95129487; PMID:7828536
A/Accession: 167431
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-233 <RES>
A/Cross-references: UNIPROT:P53563; EMBL:U04963; NID:G1004376; PIDN:AAAT7686.1; PID:G1004376
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 15.7%; Score 173.5; DB 2; Length 233;
Best Local Similarity 27.6%; Pred. No. 2.7e-08;
Matches 48; Conservative 25; Mismatches 78; Indels 23; Gaps 5;

QY 49 AEGVAAPADPEMVTLPQSSSTMVQVGRQLAIIGDDINRRYDSEFQTMQLHQPTAENAY 108
Db 68 ATGHSSSLDAREV-LP-----MAAVKQALREAGDEFELRYRAFSDLTSLQHLTPGVTV 120

QY 109 EYFTKIATSLFESGINRWGVALLGFGVRLALHVVYQHGLTGLFQGVTRFVVDFMLHHCIA 168
Db 121 QSFQVVELFRDGVNMGRIYVASSFGALCVESVDKEMQVLSRIASWATYLNDRH-LE 179

QY 169 RWIAQRGGWVAALNL-GNRP-----LNVLVVLGVVLGQFVVR 207
Db 180 PWIQENGWDTFVDLYGNNTAPESRKGQERFNRFMTGTVAGVVLGSLFSRK 233

RESULT 14
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C/Species: Cricetulus griseus (Chinese hamster)
C/Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C/Accession: JC7383
R/Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A/Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A/Reference number: JC7383
A/Contents: Ovary
A/Accession: JC7383
A/Molecule type: mRNA
A/Residues: 1-236 <TON>
A/Cross-references: UNIPROT:Q9JUV8; GB:A0271720
C/Comment: This protein has anti-apoptotic function, and supports cell survival.
C/Genetics:
A/Gene: bcl-2
C/Superfamily: bcl apoptosis regulator, inhibitory type

us-09-633-200-7.rpr

Mon Dec 6 16:29:28 2004

C;Keywords: B-cell lymphoma; ovary

Query Match 15.6%; Score 172.5; DB 2; Length 236;
 Best Local Similarity 24.4%; Pred. No. 3.4e-08;
 Matches 55; Conservative 30; Mismatches 93; Indels 47; Gaps 7;

QY 22 ASEEQVAQDTEEVFRSYVYRHHQEQ-----EAGVAAPA- 56
 Db 2 AQAGRTGYDNRREIVMKYIHKLQSGYEWVDGVDAAPLGAAPTGIFSFQPSNRTPAV 61

QY 57 --DPENVTLPLQF--SSTMGQ-----VGRQLAIGDDINRRYDSEFQTMQLHQLQPTAE 105
 Db 62 HRDMAARTSPLRPVATTGPTLSPVPVHLTLRRAGDDFSRRYRDDFAEMSSQLHLTPF 121

QY 106 NAYEYFTKIATSLFESGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVFLHH 165
 Db 122 TARGRFATVVEELFRDGVNWRIVAFEFEGGVCMCVSNREMSPLVDNIALMTETLNRH 181

QY 166 CIARWIAQRGWVAALNLGNPI-----LNLVLVLGVVLLG 201
 Db 182 -LHTWIQDNGWDFAVEL-YGFSVRELPDFSNLSKLTLLSLALVG 224

RESULT 15
 I67432
 BCU-2 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I67432
 R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equivalent bcl-2 and bcl-xL long messenger ribonucleic acid levels.
 A;Reference number: I53295; MUID:95129487; PMID:7828536
 A;Accession: I67432
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-236 <RES>
 A;Cross-references: UNIPROT:P49950; EMBL:U34964; NID:G1004378; PIDN:AAA77687.1; PID:G1004378
 C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 15.5%; Score 170.5; DB 2; Length 236;
 Best Local Similarity 23.3%; Pred. No. 5.2e-08;
 Matches 53; Conservative 30; Mismatches 93; Indels 51; Gaps 7;

QY 22 ASEEQVAQDTEEVFRSYVYRHHQEQ-----EAGVAAPA- 56
 Db 2 AQAGRTGYDNRREIVMKYIHKLQSGYEWVDGSDSAPLRRAPTGCIFSFQPSNRTPAV 61

QY 57 --DPENVTLPLQSSMGVGRQLAI-----GDDINRRYDSEFQTMQLHQLQPT 103
 Db 62 HRDTAARTSPLRP--LVANAGPALSPVPVHLLTLRRAGDDFSRRYRDDFAEMSSQLHLT 119

QY 104 AENAYEFTKIATSLFESGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVFL 163
 Db 120 PFTARGRFATVVEELFRDGVNWRIVAFEFEGGVCMCVSNREMSPLVDNIALMTETLNRH 179

QY 164 HUCIARWIAQRGWVAALNLGNPI-----VVLGVVLLG 201
 Db 180 RH-LHTWIQDNGWDFAVEL-YGFSMRPLDFSNLSKLTLLSLALVG 224

Search completed: December 6, 2004, 16:12:32
 Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: December 6, 2004, 16:11:57 ; Search time 141 Seconds
(without alignments)
533.670 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGQGFPPRCQCBPALP.....LVVLGVLLGQFVRRFFKS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	100.0	211	14	US-10-101-482-7
2	1103	100.0	211	14	US-10-101-482-10
3	1103	100.0	211	14	US-10-189-294-2
4	1103	100.0	211	14	US-10-177-293-25
5	1103	100.0	211	15	US-10-003-632C-6
6	1103	100.0	211	17	US-10-825-282-34
7	1088.5	98.7	210	14	US-10-101-482-22
8	1075	97.5	211	14	US-10-101-482-9
9	1075	97.5	211	14	US-10-101-482-11
10	625	56.7	117	14	US-10-189-294-5
11	609	55.2	116	14	US-10-189-294-5
12	236	21.4	45	9	US-09-971-980-39
13	214.5	19.4	99	15	US-10-294-445-26

14	192	17.4	205	13	US-10-087-192-1956	Sequence 1956, Appl
15	192	17.4	239	15	US-10-148-953A-4	Sequence 4, Appl
16	191	17.3	239	15	US-10-287-321-2	Sequence 2, Appl
17	190	17.2	239	8	US-08-726-211-5	Sequence 5, Appl
18	190	17.2	239	10	US-09-993-420A-8	Sequence 8, Appl
19	190	17.2	239	14	US-10-101-482-12	Sequence 12, Appl
20	190	17.2	239	14	US-10-072-830-2	Sequence 2, Appl
21	190	17.2	239	14	US-10-141-618-12	Sequence 12, Appl
22	190	17.2	239	14	US-10-053-645A-21	Sequence 21, Appl
23	190	17.2	239	14	US-10-387-961A-5	Sequence 5, Appl
24	190	17.2	239	15	US-10-003-632C-1	Sequence 1, Appl
25	190	17.2	239	15	US-10-003-632C-3	Sequence 3, Appl
26	190	17.2	239	15	US-10-148-953A-1	Sequence 1, Appl
27	190	17.2	239	15	US-10-148-953A-3	Sequence 3, Appl
28	190	17.2	239	16	US-10-450-366-4	Sequence 4, Appl
29	190	17.2	239	17	US-10-770-668-16	Sequence 16, Appl
30	190	17.2	239	17	US-10-825-282-46	Sequence 46, Appl
31	189.5	17.2	205	8	US-08-726-211-7	Sequence 7, Appl
32	189.5	17.2	205	9	US-09-952-278-4	Sequence 4, Appl
33	189.5	17.2	205	14	US-10-053-645A-23	Sequence 23, Appl
34	189.5	17.2	205	14	US-10-387-961A-7	Sequence 7, Appl
35	189.5	17.2	205	15	US-10-003-632C-2	Sequence 2, Appl
36	189.5	17.2	205	15	US-10-003-632C-11	Sequence 11, Appl
37	189	17.1	239	14	US-10-277-693A-10	Sequence 10, Appl
38	189	17.1	239	15	US-10-003-632C-10	Sequence 10, Appl
39	189	17.1	239	15	US-10-003-632C-13	Sequence 13, Appl
40	189	17.1	239	15	US-10-148-953A-2	Sequence 2, Appl
41	189	17.1	239	15	US-10-148-953A-5	Sequence 5, Appl
42	184	16.7	229	16	US-10-659-705-7	Sequence 7, Appl
43	183	16.6	36	11	US-09-828-870-14	Sequence 14, Appl
44	183	16.6	179	14	US-10-402-017-6	Sequence 6, Appl
45	182	16.5	199	14	US-10-402-017-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-101-482-7
; Sequence 7, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/101/101.482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/320.157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792

```
;
;
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-101-482-7

Query Match      100.0%; Score 1103; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGGPPPPROECGEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
DB 1 MASGGGPPPPROECGEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLMHLHICIARWIAORGGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLMHLHICIARWIAORGGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211

RESULT 2
US-10-101-482-10
; Sequence 10, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORESTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-101-482-10

Query Match      100.0%; Score 1103; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGGPPPPROECGEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
DB 1 MASGGGPPPPROECGEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLMHLHICIARWIAORGGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLMHLHICIARWIAORGGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211

RESULT 3
US-10-189-294-2
; Sequence 2, Application US/10189294
; Publication No. US20030060615A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, Michael C.
; Gibson, Helen L.
; Fitzpatrick, Paul A.
; Barr, Phillip J.
; TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA
; ENCODING THE PROTEIN, AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, THERESA A.
; STREET: 1560 Broadway, Suite 1200
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/189,294
; FILING DATE: 01-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-189-294-2

Query Match      100.0%; Score 1103; DB 14; Length 211;
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				Indels	0;
				Gaps	0;
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Db	1	MASGGCGPPRQCEGEPALPSASBEQVAQDTEEVFRSYVYRRHQEQEAEQVAAADPEM	60		
QY	61	VTLPLQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYVYFTKIATSLPE	120		
Db	61	VTLPLQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYVYFTKIATSLPE	120		
QY	121	SGINGRVALLGFGYRLALHYOHGTGELGQVTRPVVDFMLHHCIAEWIAQRGWAA	180		
Db	121	SGINGRVALLGFGYRLALHYOHGTGELGQVTRPVVDFMLHHCIAEWIAQRGWAA	180		
QY	181	NLNGKPIINVLWLGVVLLGQFVVRFFKS	211		
Db	181	NLNGKPIINVLWLGVVLLGQFVVRFFKS	211		

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RESULT 4
US-10-177-293-25
; Sequence 25, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-25

Query Match 100.0%; Score 1103; DB 14; Length 211;
Best Local Similarity 100.0%; Pred.No.8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGGPGPRGCGCEPALFASAEQVAODTEVFVFRVYRHQOQEAEQVAAPDEPM 60

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RESULT 5
US-10-003-632C-6
; Sequence 6, Application US/10003632C
; Publication No. US20040043028A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Ximei
; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or
; FILE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nuclei
; FILE REFERENCE: CEN0269
; CURRENT APPLICATION NUMBER: US/10/003,632C
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 211
; TYPE: PRM
; ORGANISM: Homo sapiens
US-10-003-632C-6

Query Match      100.0%; Score 1103; DB 15; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MASGQGPGPPRQSCGEPALPSASSEEQAQDTEEVFRSYFYRHQQEQEAGVAAPADPEM 60
Db      1  MASGQGPGPPRQSCGEPALPSASSEEQAQDTEEVFRSYFYRHQQEQEAGVAAPADPEM 60

Qy      61  VTLPLOFSSSTMGGVGRQLAIIIGDDINRRYDSEFQTMLOHLQPTAENAYEYFTKIATSLFE 120
Db      61  VTLPLOFSSSTMGGVGRQLAIIIGDDINRRYDSEFQTMLOHLQPTAENAYEYFTKIATSLFE 120

Qy      121  SGINWGRVVALLGFGYRLALHVYOHGLTGFGLGVQVTRFVDFMLHHCICARWIAQRGGWAA 180
Db      121  SGINWGRVVALLGFGYRLALHVYOHGLTGFGLGVQVTRFVDFMLHHCICARWIAQRGGWAA 180

Qy      181  LNLNGSPILNLVVLGVWILGQFVVRFFKS 211
Db      181  LNLNGSPILNLVVLGVWILGQFVVRFFKS 211

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RESULT 6
US-10-825-282-34
; Sequence 34, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29

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; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 211
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-10-825-282-34

Query Match      100.0%; Score 1103; DB 17; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGQGGPPRCGCEPALPSASEEQVAODTEEVRSYVYVRHQOEAEAGVAAPADPEM 60
DB 1 MASGQGGPPRCGCEPALPSASEEQVAODTEEVRSYVYVRHQOEAEAGVAAPADPEM 60
QY 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSFQTMQLQHOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSFQTMQLQHOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211

RESULT 7
US-10-101-482-22
; Sequence 22, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-10-101-482-9

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-10-101-482-22

Query Match      98.7%; Score 1088.5; DB 14; Length 210;
Best Local Similarity 99.5%; Pred. No. 2.3e-99;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MASGQGGPPRCGCEPALPSASEEQVAODTEEVRSYVYVRHQOEAEAGVAAPADPEM 60
DB 1 MASGQGGPPRCGCEPALPSASEEQVAODTEEVRSYVYVRHQOEAEAGVAAPADPEM 60
QY 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSFQTMQLQHOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSFQTMQLQHOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211

RESULT 8
US-10-101-482-9
; Sequence 9, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
; US-10-101-482-9
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Query Match 97.5%; Score 1075; DB 14; Length 211;
Best Local Similarity 97.2%; Pred. No. 5.1e-98;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASCGGPPRQCGEPALPSASEQVAQTEEVFRSYVYHHQOEAEAGAAAPADPEM 60
|
Db 1 MASCGGPPRQCGEPALPSASEQVAQTEEVFRSYVYHHQOEAEAGAAAPADPEM 60
|
QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPQTAENAYEYFTKIATSLPE 120
|
Db 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPQTAENAYEYFTKIATSLPE 120
|
QY 121 SGINNGRVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
|
Db 121 SGINNGRVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
|
QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
|
Db 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
|

RESULT 9
US-10-101-482-11
; Sequence 11, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101.482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-101-482-11

Query Match 97.5%; Score 1075; DB 14; Length 211;
Best Local Similarity 97.2%; Pred. No. 5.1e-98;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASCGGPPRQCGEPALPSASEQVAQTEEVFRSYVYHHQOEAEAGAAAPADPEM 60
|
Db 1 MASCGGPPRQCGEPALPSASEQVAQTEEVFRSYVYHHQOEAEAGAAAPADPEM 60
|

Db 1 MASCGGPPRQCGEPALPSASEQVAQTEEVFRSYVYHHQOEAEAGAAAPADPEM 60
|
QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPQTAENAYEYFTKIATSLPE 120
|
Db 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPQTAENAYEYFTKIATSLPE 120
|
QY 121 SGINNGRVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
|
Db 121 SGINNGRVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
|
QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
|
Db 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
|

RESULT 10
US-10-189-294-4
; Sequence 0, Application US/10189294
; Publication No. US20030060615A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, Michael C.
; Gibson, Helen L.
; Fitzpatrick, Paul A.
; Barr, Phillip J.
; TITLE OF INVENTION: A NOVEL Bak BINDING PROTEIN, DNA
; ENCODING THE PROTEIN, AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, THERESA A.
; STREET: 1560 Broadway, Suite 1200
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/189,294
; FILING DATE: 01-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: /note= "Bak (delta)2 (delta)TW"
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..117
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-189-294-4

Query Match 56.7%; Score 625; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.4e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 MGQVGRQLAIGDDINRRYDSEFQTMQLQHPQTAENAYEYFTKIATSLFESGINWGRVAA 130
|
Db 1 MGQVGRQLAIGDDINRRYDSEFQTMQLQHPQTAENAYEYFTKIATSLFESGINWGRVAA 60
|

QY 131 LLGFGYRLAHVYQGLTGFLGQVTFVVDVFLHHCIARWIAQRGWVAALNLGNP 187
Db 61 LLGFGYRLAHVYQGLTGFLGQVTFVVDVFLHHCIARWIAQRGWVAALNLGNP 117

RESULT 11
US-10-189-294-5
; Sequence 5, Application US/10189294
; Publication No. US20030060615A1
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; Gibson, Helen L.
; Fitzpatrick, Paul A.
; Barr, Philip J.
; TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, THERESA A.
; STREET: 1560 Broadway, Suite 1200
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/189,294
; APPLICATION NUMBER: US/10/189,294
; FILING DATE: 01-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..116
; OTHER INFORMATION: /note= "Bak (delta)3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-189-294-5
Query Match 55.2%; Score 609; DB 14; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.2e-52;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 MLQHLQPTAENAYEYFTKIATSLFESGINWGRVALLGFGYRLAHVYQGLTGFLGQVT 155
Db 1 MLQHLQPTAENAYEYFTKIATSLFESGINWGRVALLGFGYRLAHVYQGLTGFLGQVT 60
QY 156 RFVVDVFLHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQFVVRFFKS 211
Db 61 RFVVDVFLHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQFVVRFFKS 116

RESULT 12
US-09-971-980-39
; Sequence 39, Application US/09971980
; Patent No. US20020164349A1

; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flavivirus
; TITLE OF INVENTION: Pestiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020164349A1e1 Sequence
US-09-971-980-39
Query Match 21.4%; Score 236; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 163 LHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQFVVR 207
Db 1 LHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQFVVR 45

RESULT 13
US-10-294-445-26
; Sequence 26, Application US/10294445
; Publication No. US20040023866A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: BACTERIAL BCL-2 DOMAIN-CONTAINING
; TITLE OF INVENTION: POLYPEPTIDES, ENCODING NUCLEIC ACID MOLECULES, AND RELATED
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: P-LJ 5489
; CURRENT APPLICATION NUMBER: US/10/294,445
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/332,964
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-294-445-26
Query Match 19.4%; Score 214.5; DB 15; Length 99;
Best Local Similarity 41.7%; Pred. No. 3e-13;
Matches 40; Conservative 19; Mismatches 36; Indels 1; Gaps 1;
QY 82 GDDINRYDSEFOTMLQHLQPTAENAYEYFTKIATSLFESGINWGRVALLGFGYRLAH 141
Db 5 GDELEKRYEYFVFSMAVQLHITETARELFTQAGLFSGGINWGRVALLGFGGALAKK 64
QY 142 YIQHGLTGFLGQVTFVVDVFLHHCIARWIAQRGW 177
Db 65 LVNSAMEGLVSLRADWVVEFLKH- LAEWIQQGGW 99

RESULT 14
US-10-087-192-1956
; Sequence 1956, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.


```
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1956
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1956
```

```
Query Match 17.4%; Score 192; DB 13; Length 205;
Best Local Similarity 27.7%; Pred. No. 1.4e-10;
Matches 53; Conservative 25; Mismatches 73; Indels 40; Gaps 6;

QY 30 DTEVFRSYVYRHHQ---EQEAEGV-----AAPA-----DPEMVT 62
DB 10 DNRDIVMKYIHYKLSQRYEWDAGDVGAAPGAPAPGCISSQPGHTPHPAASRDPVART 69

QY 63 LPLO-PSSTMGOVGRQLAII-----GDDINRRYDSEFQTMLOHLOPTAENAYEY 110
DB 70 SPLQTPAAPGAAAGPALSPPVPPVHLTLRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGR 129

QY 111 FTKIATSLFESGINWGRVVALLGFGYRLALHVYQGLTGFLGQVTRFVVDFMLHHCIARW 170
DB 130 FATVVEELFRDGVNWGRIVAFPEFGVCMVEAVNREMSPLVDNIALWTEILNRH-LHTW 188

QY 171 IAORGWVAALNLGNPI-----LNVLVVLGVVLLG 201
DB 189 IQDNGGWDAFVEL-YGPSMRPLFDPSWLSLKTLLSLALVG 227
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Search completed: December 6, 2004, 16:24:07
Job time : 142 secs

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RESULT 15
US-10-148-953A-4
; Sequence 4, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: modified Bcl-2 protein
US-10-148-953A-4
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Query Match 17.4%; Score 192; DB 15; Length 239;
Best Local Similarity 26.4%; Pred. No. 1.7e-10;
Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;

QY 30 DTEVFRSYVYRHHQ---EQEAEGV-----AAPA-----DPEMVT 62
DB 10 DNRDIVMKYIHYKLSQRYEWDAGDVGAAPGAPAPGCISSQPGHTPHPAASRDPVART 69
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 15:54:19 ; Search time 152 Seconds
(without alignments)
497.973 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGQGPGRQBCGSPALP.....LVVLGVLLGQFVRRFFKS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesecp_23Sep04:.*
1: Genesecp1980s:.*
2: Genesecp1990s:.*
3: Genesecp2000s:.*
4: Genesecp2001s:.*
5: Genesecp2002s:.*
6: Genesecp2003as:.*
7: Genesecp2003bs:.*
8: Genesecp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	100.0	211	2 AAR77876	Human Cdn
2	1103	100.0	211	2 AAR81451	Aar81451 Bcl-Y apo
3	1103	100.0	211	2 AAW03668	Aaw03668 Bak prote
4	1103	100.0	211	2 AAW79534	Aaw79534 Bak polyP
5	1103	100.0	211	2 AAY05433	Aay05433 Human BAK
6	1103	100.0	211	5 ABB82374	Abb82374 Human BAK
7	1103	100.0	211	6 AAE37655	Aae37655 Bcl2 rela
8	1103	100.0	211	6 ABR47397	Abr47397 Breast ca
9	1103	100.0	211	7 ADD93300	Add93300 Human pro
10	1103	100.0	211	7 ADF60830	Adf60830 Human Bak
11	1103	100.0	211	8 ADL69726	Adl69726 Human Cdn
12	1075	97.5	211	2 AAR77877	Aar77877 Human Cdn
13	1075	97.5	211	2 AAW03669	Aaw03669 Bak-2 pro
14	946	85.8	211	8 ADP04114	Adp04114 Human col
15	829.5	75.2	208	2 AAY05432	Aay05432 Mouse BAK
16	791	71.7	152	2 AAR77879	Aar77879 Human Cdn
17	737	66.8	141	2 AAR77880	Aar77880 Human Cdn
18	625	56.7	117	2 AAW79535	Aaw79535 Truncated
19	609	55.2	116	2 AAR77881	Aar77881 Human Cdn
20	609	55.2	116	2 AAW79536	Aaw79536 Truncated
21	368	33.4	77	8 ADH18941	Adh18941 Human cel
22	284	25.7	52	4 AAB35127	Aab35127 Mammalian
23	284	25.7	52	5 AAU76550	Aau76550 Murine Ba
24	214.5	19.4	99	8 ADL17046	Adl17046 Bcl-2 dom
25	192	17.4	239	4 AAG64038	Aag64038 Human Bcl

26	191.5	17.4	232	2 AAW01020	Aaw01020 Apoptosis
27	191.5	17.4	232	2 AAW94347	Aaw94347 Human Bcl
28	191	17.3	239	2 AAW02383	Aaw02383 Human BCL
29	191	17.3	239	5 ABB05227	Abb05227 Human D34
30	191	17.3	239	7 ADF28076	Adf28076 Mutant Bc
31	190	17.2	239	1 AAF80987	Aaf80987 Sequence
32	190	17.2	239	2 AAR42312	Aar42312 Bcl-2 onc
33	190	17.2	239	2 AAR47344	Aar47344 Human onc
34	190	17.2	239	2 AAR70331	Aar70331 Human bcl
35	190	17.2	239	2 AAR71404	Aar71404 Human bcl
36	190	17.2	239	2 AAW40217	Aaw40217 Human bcl
37	190	17.2	239	2 AAW87812	Aaw87812 A human B
38	190	17.2	239	3 AAY69203	Aay69203 Amino aci
39	190	17.2	239	4 AAB48288	Aab48288 Human BCL
40	190	17.2	239	4 AAG64037	Aag64037 Human BCL
41	190	17.2	239	4 AAG64035	Aag64035 Human Bcl
42	190	17.2	239	4 AAB50537	Aab50537 Human Bcl
43	190	17.2	239	4 AAB74129	Aab74129 Human Bcl
44	190	17.2	239	4 AAE08573	Aae08573 Human Bcl
45	190	17.2	239	5 AAG31127	Aag31127 Bcl-2 ant

ALIGNMENTS

RESULT 1
AAR77876
ID AAR77876 standard; protein; 211 AA.
XX AC AAR77876;
XX AC

25-MAR-2003 (revised)
21-NOV-1995 (first entry)
XX DT
XX DT
XX XX
DE Human Cdn-1.

Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis; shock;
KW lymphoma; eczema.

OS Homo sapiens.
XX XX
FN WO9515084-A1.
XX PD
PD 08-JUN-1995.

PF 30-NOV-1994; 94WO-US013930.
XX PR
PR 30-NOV-1993; 93US-00160067.
PR 07-OCT-1994; 94US-00320157.
XX XX
(LXRB-) LXR BIOTECHNOLOGY INC.

PI Kiefer MC, Barr PJ;
XX WPI; 1995-215106/28.
DR N-PSDB; AAQ95492.

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
XX related vectors, transformed cells, proteins and antibodies, useful for
XX diagnosis and treatment e.g. of HIV infection, reperfusion injury etc.

PS Disclosure; Fig 3A-B; 66pp; English.

XX Cdn-1 cDNA was isolated from a human heart cDNA library using a
XX previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9
XX and human colon adenocarcinoma HT29 cells. Expression of Cdn-1 in WI-L2
XX lymphoblastoid cells resulted in increased cell survival in response to
XX anti-Fas-mediated apoptosis. (Updated on 25-MAR-2003 to correct FN
XX field.)

SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGCGPPROECGEPALPSASEEQVAQDTTEEVRSYVYVYRHQOEQAEGVAAPADPEM 60
DB 1 MASGCGPPROECGEPALPSASEEQVAQDTTEEVRSYVYVYRHQOEQAEGVAAPADPEM 60

QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFLHHCIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFLHHCIARWIAQRGWVAA 180

QY 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFFKS 211
DB 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFFKS 211

RESULT 2
AAR81451
ID AAR81451 standard; protein; 211 AA.
XX
AC AAR81451;
DT 02-JUL-1996 (first entry)
DE Bcl-Y apoptosis-related protein.
XX
KW Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 188..205
FT /label= C-terminal domain
FT /note= "putative membrane localisation sequence"

XX WO9605232-A1.
XX 22-FEB-1996.
XX 09-AUG-1995; 95WO-US010103.
XX 09-AUG-1994; 94US-00287427.
XX 11-OCT-1994; 94US-00321071.
XX (IMMU-) IMMUNOGEN INC.
XX Chittenden TD;
XX WPI; 1996-139648/14.
XX N-PSDB; AAT17375.

PT New isolated human Bcl-Y protein - used to develop prods. for treating
PT disorders characterised by inappropriate cell proliferation or cell
PT death.

PS Claim 3; Fig 4; 100pp; English.

XX Bcl-Y protein (AAR81451) is a member of the Bcl-2 family and can induce
XX apoptosis in cells and function as a negative regulator of Bcl-2
XX function. Bcl-Y mRNA was detected in all human tumour cell lines examined
XX and is also widely expressed in primary human tissues. It can be obtd. by
XX expression of a full-length cDNA clone (AAT17375) in pref. mammalian host
XX cells. Bcl-Y can be used to develop prods. for treating disorders
XX associated with inappropriate cell proliferation or cell death, and to
XX raise antibodies used for the diagnosis or monitoring of such disorders

XX Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGCGPPROECGEPALPSASEEQVAQDTTEEVRSYVYVYRHQOEQAEGVAAPADPEM 60
DB 1 MASGCGPPROECGEPALPSASEEQVAQDTTEEVRSYVYVYRHQOEQAEGVAAPADPEM 60

QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFLHHCIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFLHHCIARWIAQRGWVAA 180

QY 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFFKS 211
DB 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFFKS 211

RESULT 3
AAW03668
ID AAW03668 standard; protein; 211 AA.

XX
AC AAW03668;
DT 22-FEB-1997 (first entry)
DE Bak protein.

XX Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus;
XX BHRF1; fusion protein; epitope tag; drug screening; co-precipitation;
XX ELISA; immuncassay; antibody; protein interactive trapping; virucide;
XX antitumour; diagnostic.

XX Homo sapiens.

XX WO9633416-A1.

XX 24-OCT-1996.

XX 19-APR-1996; 96WO-US005639.

XX 20-APR-1995; 95US-00426529.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Barr PJ, Kiefer MC;

XX WPI; 1996-485886/48.

XX N-PSDB; AAT42138.

XX Screening for anti-viral agents - by detecting the ability of an agent to
XX disrupt the interaction of a Bak protein and a viral protein.

XX Disclosure; Fig 1; 24pp; English.

XX This Bak protein sequence represents a bcl-1 homologue which interacts
XX with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is
XX capable of modulating apoptosis. The protein may be used in complete or
XX partial form, or as an epitope tag fusion protein, in a new virucide drug
XX screening method, which involves combination of Bak protein and a viral
XX protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for
XX disruption of the interaction, e.g. by co-precipitation, protein
XX interactive trapping or ELISA. Interaction of Bak and viral proteins
XX allows viral replication or latency in the absence of apoptosis.
XX Compounds which inhibit the interaction may be used as virucide,
XX antitumour or diagnostic agents

XX Sequence 211 AA;

Query Match

100.0%; Score 1103; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQGGPPRQCGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAAPADPEM 60
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 1 MASQGGPPRQCGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAAPADPEM 60

QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120
Cc proteins that control apoptosis is a major focal point in the treatment
Cc of heart disease, viral infection and cancer

Db 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVALLGFGYRLALHVVYQHGTLGPGQVTRFVDFMLHHCIAHWIAQRGWVAA 180
Cc binding between Bak and BbP, as well as diagnostic and therapeutic
Cc methods utilising BbP. The invention also encompasses novel Bak-derived
Cc peptides, designated BbP binding domains (BbPBDs), and novel nucleotides,
Cc designated BbPBD-1 and BbPBD-2 encoding the peptides, which are involved
Cc in the interaction between Bak and BbP, and which have been characterised
Cc as important death domains of Bak. Modulation of the interaction between
Cc proteins that control apoptosis is a major focal point in the treatment
Cc of heart disease, viral infection and cancer

Db 121 SGINWGRVALLGFGYRLALHVVYQHGTLGPGQVTRFVDFMLHHCIAHWIAQRGWVAA 180

QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
Cc Sequence 211 AA;

Db 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 4
AAW79534
ID AAW79534 standard; protein; 211 AA.
XX
AC AAW79534;
XX
DT 11-JAN-1999 (first entry)
XX
DE Bak polypeptide.
XX
KW Bak; bak binding protein; BbP; BbPBD-1; BbPBD-2; Bcl-2; apoptosis;
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

OS Homo sapiens.

XX
FH Key
FT Peptide
FT 103.126
FT /label= BbPBD-1
FT /note= "Claim 36"
FT Peptide
FT 138.156
FT /label= BbPBD-2
FT /note= "Claim 62"
XX
PN WO9841626-A1.
XX
PD 24-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US004079.
XX
PR 20-MAR-1997; 97US-0041328P.
PR 09-JAN-1998; 98US-0071097P.
XX
PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI Kiefer MC, Fitzpatrick PA, Gibson HL, Barr PU;
XX
DR WPI; 1998-521220/44.
DR N-PSDB; AAV61498.
XX
PT New Bak-binding protein and related nucleic acid, vectors, transformed
Cc cells and antibodies - are useful for modulation of apoptosis in cancer,
Cc neuro-degeneration etc., also peptide fragments of Bak that interact with
Cc the protein.

PS Disclosure; Fig 2A-C; 77pp; English.

XX
CC This is the amino acid sequence of human Bak, a member of the Bcl-2
Cc family that is expressed in heart and other tissues, and which is capable
Cc of either killing cells, or actively protecting cells from apoptosis,
Cc depending on how it interacts with other cellular proteins. A nucleotide
Cc sequence (see AAV61498) encoding Bak is provided. The invention relates
Cc to a novel Bak binding protein (BbP, see AAW79537), the gene encoding BbP

(see AAV61499), methods for detecting substances that alter the specific
Cc binding between Bak and BbP, as well as diagnostic and therapeutic
Cc methods utilising BbP. The invention also encompasses novel Bak-derived
Cc peptides, designated BbP binding domains (BbPBDs), and novel nucleotides,
Cc designated BbPBD-1 and BbPBD-2 encoding the peptides, which are involved
Cc in the interaction between Bak and BbP, and which have been characterised
Cc as important death domains of Bak. Modulation of the interaction between
Cc proteins that control apoptosis is a major focal point in the treatment
Cc of heart disease, viral infection and cancer

XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQGGPPRQCGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAAPADPEM 60
Cc
Db 1 MASQGGPPRQCGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAEAGVAAAPADPEM 60

QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120
Cc
Db 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVALLGFGYRLALHVVYQHGTLGPGQVTRFVDFMLHHCIAHWIAQRGWVAA 180
Cc
Db 121 SGINWGRVALLGFGYRLALHVVYQHGTLGPGQVTRFVDFMLHHCIAHWIAQRGWVAA 180

QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
Cc
Db 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 5
AAW05433
ID AAW05433 standard; peptide; 211 AA.
XX
AC AAW05433;
XX
DT 02-JUL-1999 (first entry)
XX
DE Human BAK protein sequence.
XX
KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
Cc apoptosis promoter; cancer cell; virus infected cell; inflammation;
Cc autacatibody producing cell; cancer; lymphoproliferative condition;
Cc arthritis; autoimmune disease; therapy.

OS Homo sapiens.

XX
PN WO9916787-A1.
XX
PD 08-APR-1999.
XX
PF 22-SEP-1998; 98WO-US019765.
XX
PR 26-SEP-1997; 97US-0060133P.
PR 07-OCT-1997; 97US-00946039.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1999-255058/21.
XX
PT Bcl homology domain 3 polypeptide.
XX
PS Disclosure; Fig 21b; 104pp; English.

XX
CC This sequence represents the human BAK protein. The invention relates to
Cc a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member
Cc of the BCL-2 family. The BH3 polypeptide can be used in a method for
Cc promoting apoptosis in a target cell, especially where the cell is a

CC cancer cell a virus infected cell or an autoantibody producing cell. The
 CC BH3 polypeptide can be used in therapeutic compositions for treating
 CC disease including cancer, other lymphoproliferative conditions,
 CC arthritis, inflammation, and autoimmune diseases, which may result from
 CC the down regulation of cell death regulation
 XX
 SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.4e-112;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGGGPPPPQCGPAPLPSASEEQVADTEVFYSYVYRHHQOEAGVAAAPADPEM 60
 DB 1 MASGGGPPPPQCGPAPLPSASEEQVADTEVFYSYVYRHHQOEAGVAAAPADPEM 60
 QY 61 VTLPLOPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMLOHQAENAYEYFTKIATSLPE 120
 DB 61 VTLPLOPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMLOHQAENAYEYFTKIATSLPE 120
 QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLHHCIAEWIAQRGWVAA 180
 DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLHHCIAEWIAQRGWVAA 180
 QY 181 LNLNGPILNLVNLVGLGVLGQFVVRFFKS 211
 DB 181 LNLNGPILNLVNLVGLGQFVVRFFKS 211

RESULT 6
 ABB82374
 ID ABB82374 standard; protein; 211 AA.
 XX
 AC ABB82374;
 DT 08-JAN-2003 (first entry)
 XX
 DE Human BAK protein sequence.
 XX
 KW BAK; Mill; cytostatic; neuroprotective; nootropic; cerebroprotective;
 KW apoptosis; human.
 XX
 OS Homo sapiens.
 XX
 FN WO200274908-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 04-MAR-2002; 2002WO-US006757.
 XX
 PR 02-MAR-2001; 2001US-0273091P.
 XX
 FA (MDS-) MDS PROTEOMICS INC.
 XX
 PI Mcfadden G, Moran MF;
 XX
 WIPI; 2002-740855/80.
 XX
 DR
 XX
 FT Identifying agents which may be potentially pro-apoptotic or anti-
 FT apoptotic for treating acute and chronic neurodegenerative diseases,
 PT comprises determining the effect of the test agent on complexes of BAK
 PT and/or M1L1 proteins.
 XX
 PS Disclosure; Fig 11; 83pp; English.
 XX
 CC The invention relates to identifying agents which may be potentially pro-
 CC -apoptotic or anti-apoptotic which involves determining the effect of a
 CC test agent on the complexes of BAK and/or M1L1 proteins. The methods are
 CC useful for identifying agents which may be potentially pro-apoptotic or
 CC anti-apoptotic and for identifying M1L1-interacting polypeptides, and in
 CC conducting a target or drug discovery system. The methods are useful for
 CC identifying agents capable of inhibiting M1L1 activity or which can mimic
 CC the activity of M1L1 by inhibiting the activity of BAK and which are

CC therefore anti-apoptotic agents. Agents identified by the method as
 CC involved in regulation of apoptosis may be used in the development of
 CC therapeutic agents and methods, and drug screening assays, and in
 CC increasing the sensitivity of cancer cells to chemotherapeutic treatment.
 CC Therapeutic applications of apoptosis manipulation include treatment of
 CC acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or
 CC Huntington's disease by drugs, and sensitization of cancer cells for drug
 CC /radiation-induced apoptosis by modulation of survival signals and viral
 CC transfer of apoptosis promoting genes. The present sequence represents a
 CC human BAK protein
 XX
 SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 5; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.4e-112;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGGGPPPPQCGPAPLPSASEEQVADTEVFYSYVYRHHQOEAGVAAAPADPEM 60
 DB 1 MASGGGPPPPQCGPAPLPSASEEQVADTEVFYSYVYRHHQOEAGVAAAPADPEM 60
 QY 61 VTLPLOPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMLOHQAENAYEYFTKIATSLPE 120
 DB 61 VTLPLOPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMLOHQAENAYEYFTKIATSLPE 120
 QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLHHCIAEWIAQRGWVAA 180
 DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDVFLHHCIAEWIAQRGWVAA 180
 QY 181 LNLNGPILNLVNLVGLGVLGQFVVRFFKS 211
 DB 181 LNLNGPILNLVNLVGLGVLGQFVVRFFKS 211

RESULT 7
 AAE37655
 ID AAE37655 standard; protein; 211 AA.
 XX
 AC AAE37655;
 DT 27-AUG-2003 (first entry)
 XX
 DE Bcl2 related protein #6.
 XX
 KW Bcl2 related protein; growth; protein expression.
 XX
 OS Unidentified.
 XX
 FN WO2003040374-A1.
 XX
 PD 15-MAY-2003..
 XX
 PF 02-NOV-2001; 2001WO-US045553.
 XX
 PR 02-NOV-2001; 2001WO-US045553.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Lee C, Ly C, Moore G, Shi X;
 XX
 DR WPI; 2003-441576/41.
 XX
 PT New protein expression enhancing Bcl2 related nucleic acid for producing
 PT commercially useful amounts of expressed protein, comprises a nucleic
 PT acid that encodes an expressible protein or at least one Bcl2 related
 PT protein.
 XX
 PS Disclosure; Page 52-53; 54pp; English.
 XX
 CC The invention relates to methods and compositions for enhanced protein
 CC expression and/or growth of cultured cells using co-transcription of at
 CC least one Bcl2 related protein encoding nucleic acid molecules. The
 CC invention is useful in providing enhanced growth of and/or protein

CC production from cultured mammalian host cells used for the production of
CC commercially useful amounts of expressed protein. The present sequence is
CC Bcl2 related protein
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQGGPPRQECGEPALESAGEQVAQDTEEVFRSVYFRHQEQEAGVAAAPADPEM 60
DB 1 MASQGGPPRQECGEPALESAGEQVAQDTEEVFRSVYFRHQEQEAGVAAAPADPEM 60
QY 61 VTLPQSSSTMVGQVGRQLAIGDDINRRYDSEFTMLQHLQPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQSSSTMVGQVGRQLAIGDDINRRYDSEFTMLQHLQPTAENAYEYFTKIATSLFE 120
QY 121 SGINMGVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180
DB 121 SGINMGVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180
QY 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 8

ABR47397
ID ABR47397 standard; protein; 211 AA.

AC ABR47397;

XX 12-JUN-2003 (first entry)

DT Breast cancer associated protein sequence SEQ ID NO:25.

DE Human; breast cancer; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003004989-A2.

XX 16-JAN-2003.

XX 21-JUN-2002; 2002WO-US019669.

XX 21-JUN-2001; 2001US-0299887P.

XX 27-JUN-2001; 2001US-0301572P.

XX 18-JUL-2001; 2001US-0306501P.

XX 25-SEP-2001; 2001US-0325002P.

XX 05-MAR-2002; 2002US-0362585P.

XX 14-MAY-2002; 2002US-0380391P.

XX (MILL-) MILLENIUM PHARM INC.

XX Lillie J, Cannavarapu M, Glatk K, Hoersch S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Puzstai L, Meric F, Sahin A, Mills GB;

XX WPI; 2003-210381/20.
DR N-PSDB; ACC50088.

XX Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.

XX Claim 1; SEQ ID NO 25; 128pp; English.

XX The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of

CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 6; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.4e-112;

Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQGGPPRQECGEPALESAGEQVAQDTEEVFRSVYFRHQEQEAGVAAAPADPEM 60

DB 1 MASQGGPPRQECGEPALESAGEQVAQDTEEVFRSVYFRHQEQEAGVAAAPADPEM 60

QY 61 VTLPQSSSTMVGQVGRQLAIGDDINRRYDSEFTMLQHLQPTAENAYEYFTKIATSLFE 120

DB 61 VTLPQSSSTMVGQVGRQLAIGDDINRRYDSEFTMLQHLQPTAENAYEYFTKIATSLFE 120

QY 121 SGINMGVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180

DB 121 SGINMGVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180

QY 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

DB 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 9

ADD93300

ID ADD93300 standard; protein; 211 AA.

XX ADD93300;

XX 29-JAN-2004 (first entry)

XX Human pro-apoptotic protein Bak.

XX Human; Bak; cytostatic; apoptosis

XX Homo sapiens.

XX WO2003062828-A2.

XX 31-JUL-2003.

XX 17-JAN-2003; 2003WO-GB000162.

XX 17-JAN-2002; 2002GB-00000971.

XX (UYMA-) UNIV VICTORIA MANCHESTER.

XX Griffiths GJ;

XX WPI; 2003-748015/70.

XX Determining potential effect of chemotherapeutic agents, useful for

PT treating cancer, from their ability to induce conformational change in

PT Bak protein.

XX Disclosure; SEQ ID NO 1; 16pp; English.

XX The present sequence is the protein sequence of the human pro-apoptotic

CC protein, Bak. A conformational change in the Bak protein is used in the

CC method of the invention for determining the potential effectiveness of a

CC chemotherapeutic compound for treating cancerous cells in a human or

CC animal patient. The method involves: (i) exposing a sample of the

CC cancerous cells taken from the patient to a chemotherapeutic compound, or

CC combination of compounds; and (ii) assaying for a conformational change
 CC in the Bak protein of the cells. The conformational change is preferably
 CC determined at the N-terminus of Bak or in its BHI domain, particularly
 CC using a specific binding partner, such as an antibody, for the
 CC conformationally altered protein. Conformational change in Bak is a very
 CC early (and general) indicator of commitment to apoptosis occurring
 CC before caspase activation, nuclear condensation or cellular blebbing, and
 CC is caused by agents that induce apoptosis by different mechanisms.
 CC Detecting commitment to apoptosis is a more accurate indicator of
 CC activity than cell death and the present method is quicker and simpler
 CC than known clonogenic assays.

XX Sequence 211 AA;
 SQ
 Query Match 100.0%; Score 1103; DB 7; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.4e-112;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFPSYVYRHHQOEAGVAAAPADPEM 60
 Db 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFPSYVYRHHQOEAGVAAAPADPEM 60
 Qy 61 VTLPQSPSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPDAENAYEYFTKIATSLFE 120
 Db 61 VTLPQSPSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPDAENAYEYFTKIATSLFE 120
 Qy 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDMLHHCIARWIAQRGWVAA 180
 Db 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDMLHHCIARWIAQRGWVAA 180
 Qy 181 LNLGNGPILNLVVLGVLLGQFVWRFFKS 211
 Db 181 LNLGNGPILNLVVLGVLLGQFVWRFFKS 211

RESULT 10
 ADF60830
 ID ADF60830 standard; protein; 211 AA.
 AC ADF60830;
 DT 12-FEB-2004 (first entry)
 DE Human Bak #SEQ ID 1.
 XX Chemotherapeutic; anti-apoptotic; Bak; Bcl-2; Bcl-XL; cancer; human.
 XX Homo sapiens.
 XX WO2003062829-A2.
 XX 31-JUL-2003.
 XX 17-JAN-2003; 2003WO-GB000185.
 XX 17-JAN-2002; 2002GB-00000970.
 XX (UYMA-) UNIV VICTORIA MANCHESTER.
 XX Griffiths GJ;
 XX WPI; 2003-902664/82.
 XX Detecting or screening for chemotherapeutic activity, useful for treating
 XX cancer, from induction of modifications in Bak protein in cells over
 XX expressing anti-apoptotic protein.
 XX Disclosure; Page 3; 32pp; English.
 XX The invention relates to a method for detecting a chemotherapeutic
 XX activity in a compound other than an etoposide, or in a combination of
 XX compounds. In the method of the invention, a cell that over expresses an
 XX anti-apoptotic protein is treated with at least one compound, and any

CC change in the conformation of cellular Bak, indicative of
 CC chemotherapeutic activity, is detected. The anti-apoptotic protein is Bcl
 CC -2 or Bcl-XL, and is over expressed by transfecting the cells with a
 CC pcDNA3.1 vector that contains the anti-apoptotic-expressing sequence
 CC under control of the cytomegalovirus promoter. The method of the
 CC invention is used to identify, or screen for, chemotherapeutic agents for
 CC the treatment of cancer. The current sequence represents the human Bak
 CC amino acid sequence.

XX Sequence 211 AA;
 SQ
 Query Match 100.0%; Score 1103; DB 7; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.4e-112;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFPSYVYRHHQOEAGVAAAPADPEM 60
 Db 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFPSYVYRHHQOEAGVAAAPADPEM 60
 Qy 61 VTLPQSPSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPDAENAYEYFTKIATSLFE 120
 Db 61 VTLPQSPSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPDAENAYEYFTKIATSLFE 120
 Qy 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDMLHHCIARWIAQRGWVAA 180
 Db 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDMLHHCIARWIAQRGWVAA 180
 Qy 181 LNLGNGPILNLVVLGVLLGQFVWRFFKS 211
 Db 181 LNLGNGPILNLVVLGVLLGQFVWRFFKS 211

RESULT 11
 ADF69726
 ID ADF69726 standard; protein; 211 AA.
 AC ADF69726;
 DT 20-MAY-2004 (first entry)
 DE Human Bcl2 related protein #6.
 XX Bcl2 related protein; therapeutic protein; human.
 XX Homo sapiens.
 XX US2004043028-A1.
 XX 04-MAR-2004.
 XX 02-NOV-2001; 2001US-00003632.
 XX 02-NOV-2001; 2001US-00003632.
 XX (LEEC/) LEE C.
 XX (SHIX/) SHI X.
 XX (LYCC/) LY C.
 XX (MOOR/) MOORE G.
 XX Lee C, Shi X, Ly C, Moore G;
 XX WPI; 2004-225672/21.
 XX New Bcl2 encoding nucleic acids for enhancing growth and/or production of
 XX therapeutic or diagnostic proteins from cultured mammalian host cells.
 XX Disclosure; SEQ ID NO 6; 42pp; English.
 XX The invention relates to a protein expression enhancing Bcl2 related
 XX nucleic acid comprising a first nucleic acid encoding at least one
 XX expressible protein and a second nucleic acid encoding at least one Bcl2
 XX related protein, where expression of the expressible protein is enhanced
 XX by transcription or translation of the second nucleic acid. The

CC composition and methods are useful for enhancing growth and/or production
CC of therapeutic or diagnostic proteins from cultured mammalian host cells.
CC The present sequence is human Bcl2 related protein.
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 8; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASQGGPPRQCEGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAGVAAAPADPEM 60
DB 1 MASQGGPPRQCEGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAGVAAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIAEWIAQRGWVAA 180
DB 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIAEWIAQRGWVAA 180
QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 12

AAR77877
ID AAR77877 standard; protein; 211 AA.

XX AAR77877;

XX 25-MAR-2003 (revised)

XX 21-NOV-1995 (first entry)

XX Human Cdn-2.

XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
XX autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock;
XX lymphoma; eczema.

XX Homo sapiens.

XX WO9515084-A1.

XX 08-JUN-1995.

XX 30-NOV-1994; 94WO-US013930.

XX 30-NOV-1993; 93US-00160067.

XX 07-OCT-1994; 94US-00320157.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Kiefer MC, Barr PJ;

XX WPI; 1995-215106/28.

XX N-PSDB; AAQ95493.

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
XX related vectors, transformed cells, proteins and antibodies, useful for
XX diagnosis and treatment e.g. of HIV infection, reperfusion injury etc.

XX Disclosure; Fig 5D-E; 66pp; English.

XX Cdn-2 cDNA was isolated from a human placental genomic library using a 950
XX bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell
XX FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein
XX displayed 97% amino acid identity with Cdn-1 (AAR77876). (Updated on 25-
XX MAR-2003 to correct PN field.)

XX Sequence 211 AA;

Query Match 97.5%; Score 1075; DB 2; Length 211;
Best Local Similarity 97.2%; Pred. No. 1.7e-109;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MASQGGPPRQCEGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAGVAAAPADPEM 60
DB 1 MASQGGPPRQCEGEPALPSAEEQVAQDTEEVFRSYVYRHHQOEAGVAAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIAEWIAQRGWVAA 180
DB 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIAEWIAQRGWVAA 180
QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 13

AAW03669

ID AAW03669 standard; protein; 211 AA.

XX AAW03669;

XX 22-FEB-1997 (first entry)

XX Bak-2 protein.

XX Human; Bak-2; apoptosis; latency; virus replication; Epstein-Barr virus;
XX BHRF1; fusion protein; epitope tag; drug screening; co-precipitation;
XX ELISA; immunoassay; antibody; protein interactive trapping; virucide;
XX antitumour; diagnostic.

XX Homo sapiens.

XX WO9633416-A1.

XX 24-OCT-1996.

XX 19-APR-1996; 96WO-US005639.

XX 20-APR-1995; 95US-00426529.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Barr PJ, Kiefer MC;

XX WPI; 1996-485886/48.

XX N-PSDB; AAT42139.

XX Screening for anti-viral agents - by detecting the ability of an agent to
XX disrupt the interaction of a Bak protein and a viral protein.

XX Disclosure; Fig 2; 24pp; English.

XX This Bak-2 protein sequence represents a bcl-1 homologue which interacts
XX with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is
XX capable of modulating apoptosis. The protein may be used in complete or
XX partial form, or as an epitope tag fusion protein, in a new virucide drug
XX screening method, which involves combination of Bak-2 protein and a viral
XX protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for
XX disruption of the interaction, e.g. by co-precipitation, protein
XX interactive trapping or ELISA. Interaction of Bak-2 and viral proteins
XX allows viral replication or latency in the absence of apoptosis.
XX Compounds which inhibit the interaction may be used as virucide,
XX antitumour or diagnostic agents

XX Sequence 211 AA;

Query Match 97.5%; Score 1075; DB 2; Length 211;
Best Local Similarity 97.2%; Pred. No. 1.7e-109;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGPGPPROECGEPALPSASEEQVADTEEVFRSYYVYFHQOEQAEGVAAPADPEM 60
DB 1 MASGGPGPPROECGEPALPSASEEQVADTEEVFRSYYVYFHQOEQAEGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINNGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVAA 180
DB 121 SGINNGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVAA 180
QY 181 LNLGSPILNLVLGVLGQVVRFFKS 211
DB 181 LNLGSPILNLVLGVLGQVVRFFKS 211

RESULT 14
ADP04114
ID ADP04114 standard; protein; 211 AA.
XX AC ADP04114;
XX DT 09-SEP-2004 (first entry)
XX DE Human colon specific protein SEQ ID NO:95.
XX KW human; colon specific nucleic acid; CSNA; colon specific protein; CSP;
XX KW cytostatic; vaccine; gene therapy; colon cancer.
XX OS Homo sapiens.
XX PN WO2004050858-A2.
XX PD 17-JUN-2004.
XX PF 04-DEC-2003; 2003WO-US038808.
XX PR 04-DEC-2002; 2002US-0431133P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Rodriguez M, Burcham TS;
XX WPI; 2004-480622/45.
XX DR Novel colon specific protein derived from normal and neoplastic colon
XX PT cell, useful as vaccine in treating colon cancer and in identifying,
XX PT diagnosing, monitoring, staging, imaging colon cancer and non-cancerous
XX PT disease state in colon.
XX PS Claim 12; SEQ ID NO 95; 655pp; English.
XX CC The invention relates to a novel colon specific protein (CSP) (I), and
XX CC the nucleic acid encoding it. A CSP of the invention has cytostatic
XX CC activity, and may have use in a vaccine, and in gene therapy. The CSP is
XX CC useful for determining the presence of a colon specific protein in a
XX CC sample. The nucleic acid encoding the CSP is useful for determining the
XX CC presence of a colon specific nucleic acid (CSNA) in a sample. The CSP and
XX CC CSNA are useful for diagnosing or monitoring the presence and metastases
XX CC of colon cancer in a patient. The method of administering a composition
XX CC comprising a CSP or CSNA is useful for treating a patient with colon
XX CC cancer. The CSP and CSNA are useful as vaccine for treating colon cancer
XX CC and non-cancerous disease states in colon. The present sequence
XX CC represents a CSP of the invention.
XX SQ Sequence 211 AA;
Query Match 85.8%; Score 946; DB 8; Length 211;

Best Local Similarity 97.8%; Pred. No. 2.7e-95;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MASGGPGPPROECGEPALPSASEEQVADTEEVFRSYYVYFHQOEQAEGVAAPADPEM 60
DB 1 MASGGPGPPROECGEPALPSASEEQVADTEEVFRSYYVYFHQOEQAEGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINNGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVAA 180
DB 121 SGINNGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVSI 180
QY 181 LNL 183
DB 181 QGL 183

RESULT 15
RAY05432
ID AAY05432 standard; peptide; 208 AA.
XX AC AAY05432;
XX DT 02-JUL-1999 (first entry)
XX DE Mouse BAK protein sequence.
XX KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
XX KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
XX KW autoantibody producing cell; cancer; lymphoproliferative condition;
XX KW arthritis; autoimmune disease; therapy.
XX OS Mus sp.
XX PN WO9916787-A1.
XX PD 08-APR-1999.
XX PF 22-SEP-1998; 98WO-US019765.
XX PR 26-SEP-1997; 97US-0060133P.
XX PR 07-OCT-1997; 97US-00946039.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Korsmeyer SJ;
XX WPI; 1999-255058/21.
XX DR Bcl homology domain 3 polypeptide.
XX PT Disclosure; Fig 21b; 104pp; English.
XX PS This sequence represents the murine BAK protein. The invention relates to
XX CC a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member
XX CC of the BCL-2 family. The BH3 polypeptide can be used in a method for
XX CC promoting apoptosis in a target cell, especially where the cell is a
XX CC cancer cell a virus infected cell or an autoantibody producing cell. The
XX CC BH3 polypeptide can be used in therapeutic compositions for treating
XX CC disease including cancer, other lymphoproliferative conditions,
XX CC arthritis, inflammation, and autoimmune diseases, which may result from
XX CC the down regulation of cell death regulation
XX SQ Sequence 208 AA;
Query Match 75.2%; Score 829.5; DB 2; Length 208;
Best Local Similarity 76.3%; Pred. No. 1.7e-82;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

QY 1 MASGGPGPPROECGEPALPSASEEQVADTEEVFRSYYVYFHQOEQAEGVAAPADPEM 60

Db	1	MASQGGPPKVGCDSE--PSPSEQVAQTEEVFRSYVYLHQOQETQG-RPPANPEM	57
Qy	61	VTLEPQFSSTWQVGRQALAIIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFE	120
Db	58	DNLEPFPNSILGQVGRQALIGDDINRRYDTEFQNLLEQLQPTAGNAYELFTKIAGSLFK	117
Qy	121	SGINWGRVALLGFGYELALHVYQHGTLTGQVTRFVVDFMLHHCIAHWIAORGWVAA	180
Db	118	SGISWGRVALLGFGYELALVYVQGLTGFLGQVTCFLADIILHHYIARWIAORGWVAA	177
Qy	181	LNIGNPILNVVLGVLLGQFVVRFPKS	211
Db	178	LNLRDPILTVMVIFGVLLGQFVVRFPKS	208

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